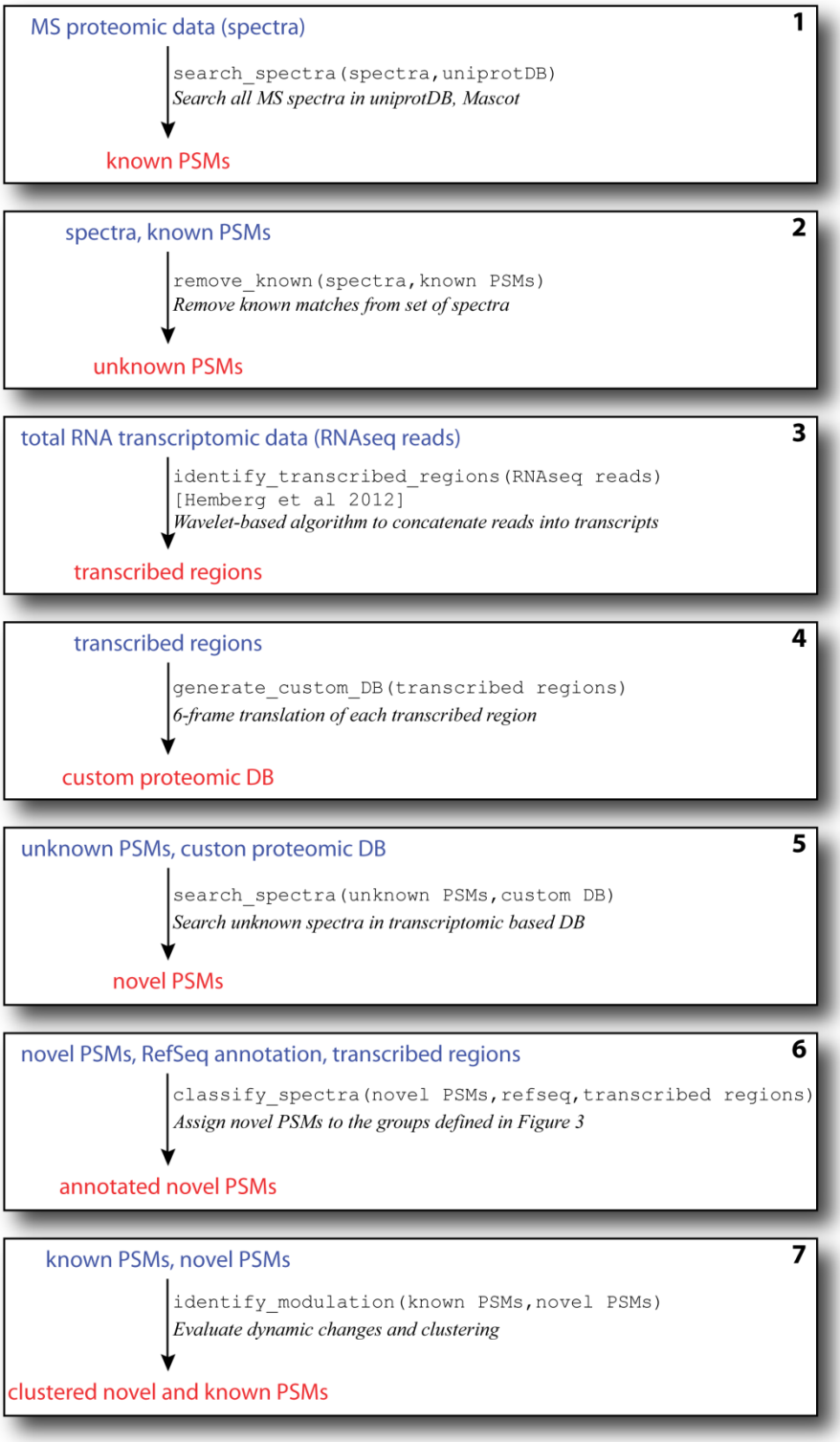
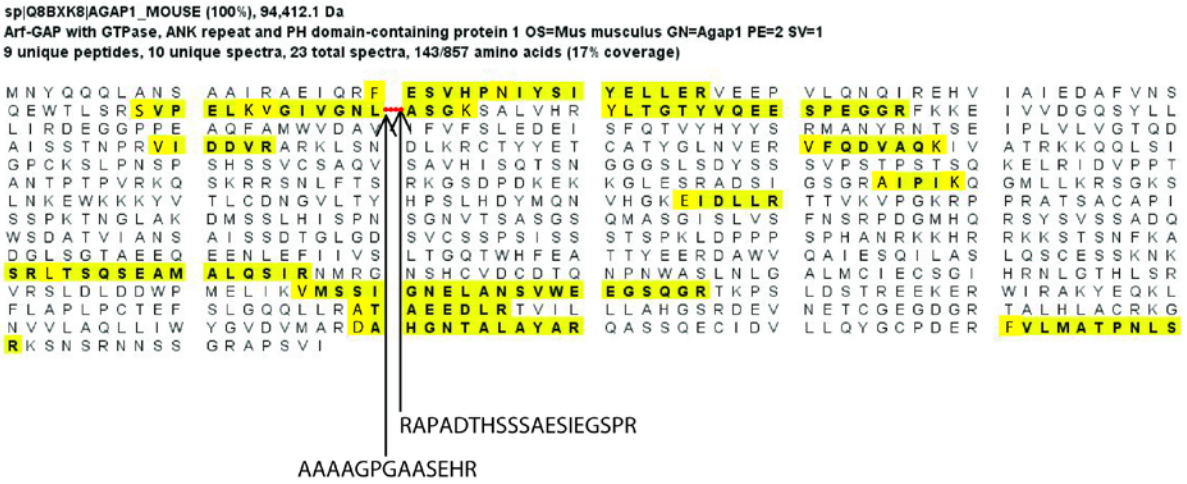
Supplementary Figure 1 **Steen**

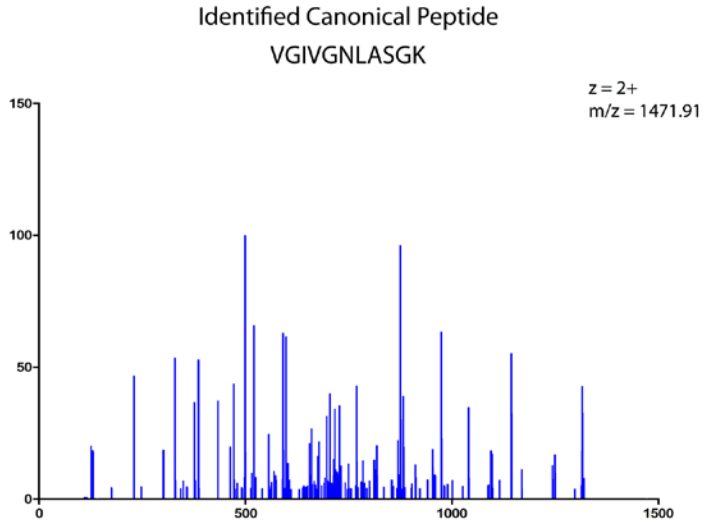


Supplementary Figure 1. Pseudocode outlining of the computational algorithm. Pseudocode outlining the main steps of our procedure for detecting unannotated translation products. Steps 1

and 5 rely on published search tools such as Mascot or Sequest, as well as step 7. Steps 2 and 4 are straightforward. The source-code for our transcript-calling algorithm is available at klab.tch.harvard.edu. We are currently in the process of developing a streamlined software tool which will enable users to search for novel translation products from RNA-seq and MS data-sets.

A

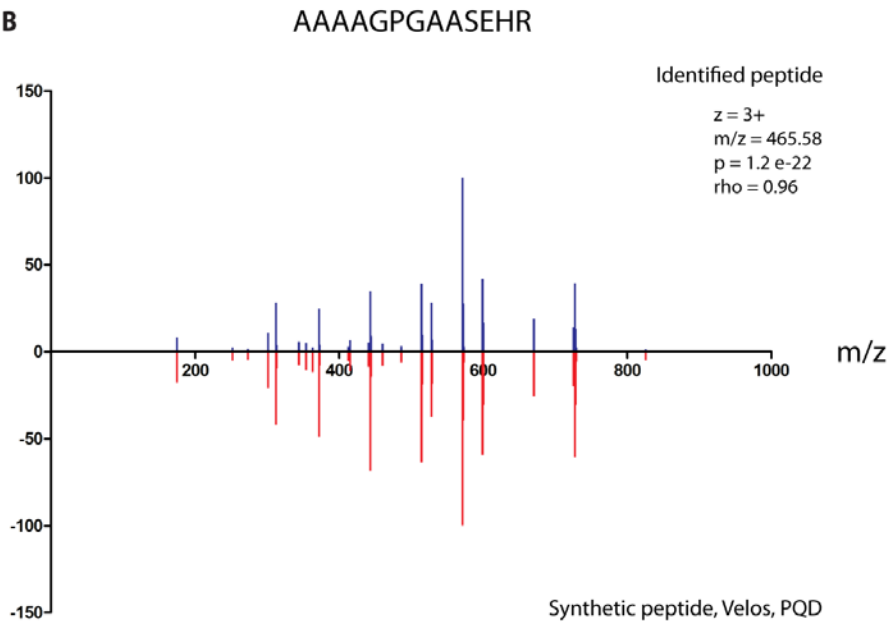




Fragmentation Table

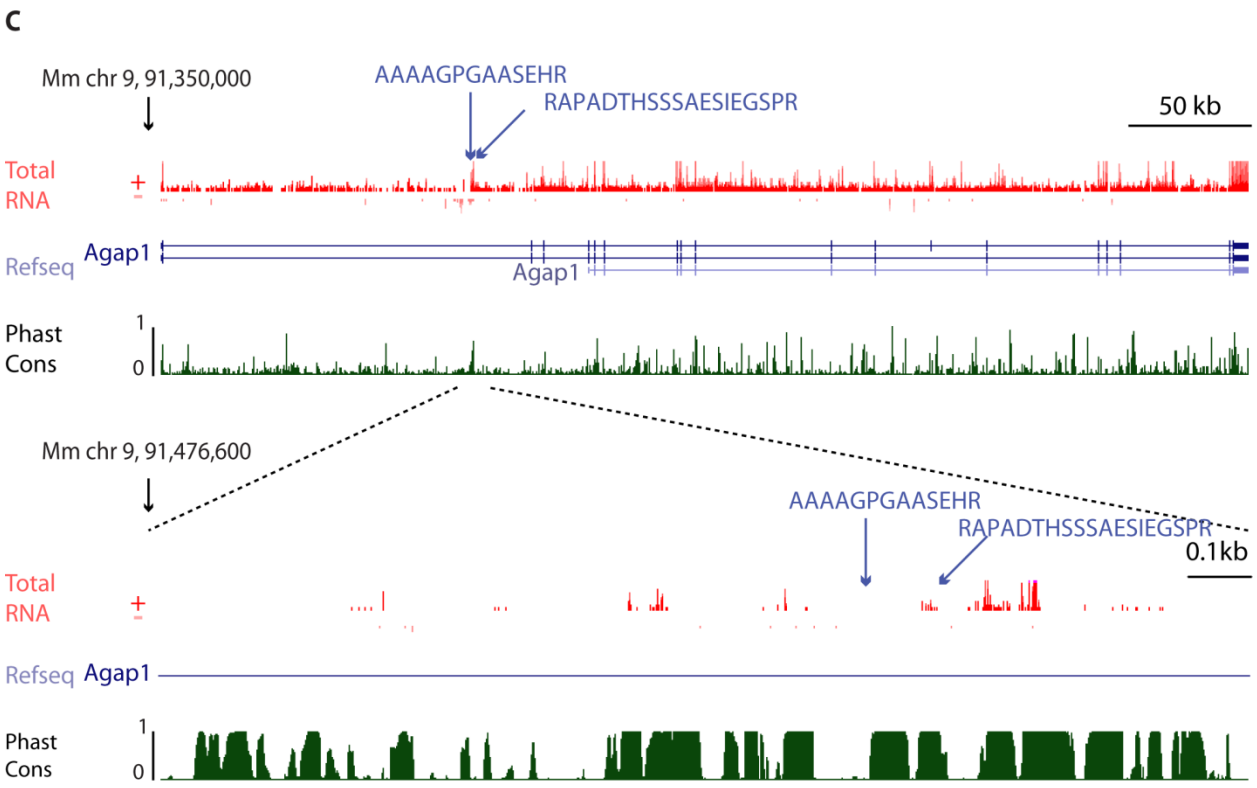
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	329.24				V+229	1,472.92	736.96	1,455.89	1,454.91	11
2	386.26				G	1,144.69	572.85	1,127.66	1,126.68	10
3	499.34				I	1,087.67	544.34	1,070.64	1,069.66	9
4	598.41				V	974.58	487.8	957.56	956.57	8
5	655.43				G	875.51	438.26	858.49	857.5	7
6	769.48	385.24	752.45		N	818.49	409.75	801.47	800.48	6
7	882.56	441.78	865.53		L	704.45		687.42	686.44	5
8	953.6	477.3	936.57		A	591.37		574.34	573.36	4
9	1,040.63	520.82	1,023.60	1,022.62	S	520.33		503.3	502.32	3
10	1,097.65	549.33	1,080.63	1,079.64	G	433.3		416.27		2
11	1,472.92	736.96	1,455.89	1,454.91	K+229	376.28		359.25		1

B

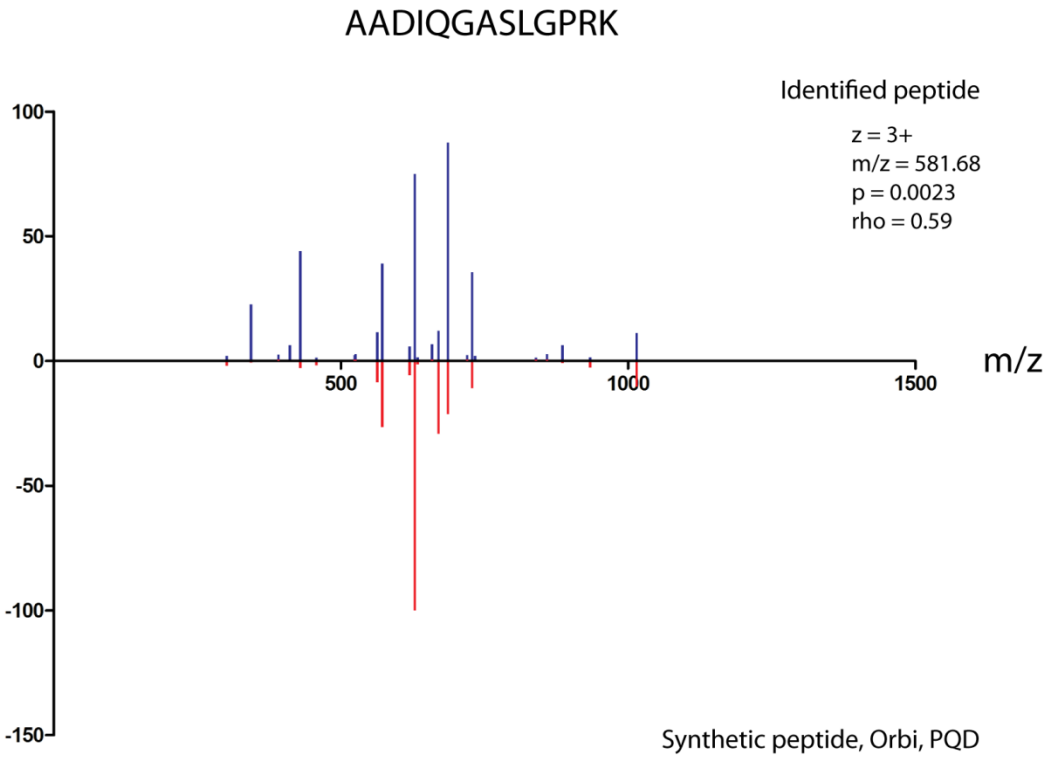


Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	301.21	151.11	A+229	1,394.73	697.87	13
2	372.24	186.63	A	1,094.53	547.77	12
3	443.28	222.14	A	1,023.50	512.25	11
4	514.32	257.66	A	952.46	476.73	10
5	571.34	286.17	G	881.42	441.21	9
6	668.39	334.7	P	824.4	412.7	8
7	725.41	363.21	G	727.35	364.18	7
8	796.45	398.73	A	670.33	335.67	6
9	867.49	434.25	A	599.29	300.15	5
10	954.52	477.76	S	528.25	264.63	4
11	1,083.56	542.29	E	441.22	221.11	3
12	1,220.62	610.81	H	312.18	156.59	2
13	1,394.73	697.87	R	175.12	88.06	1



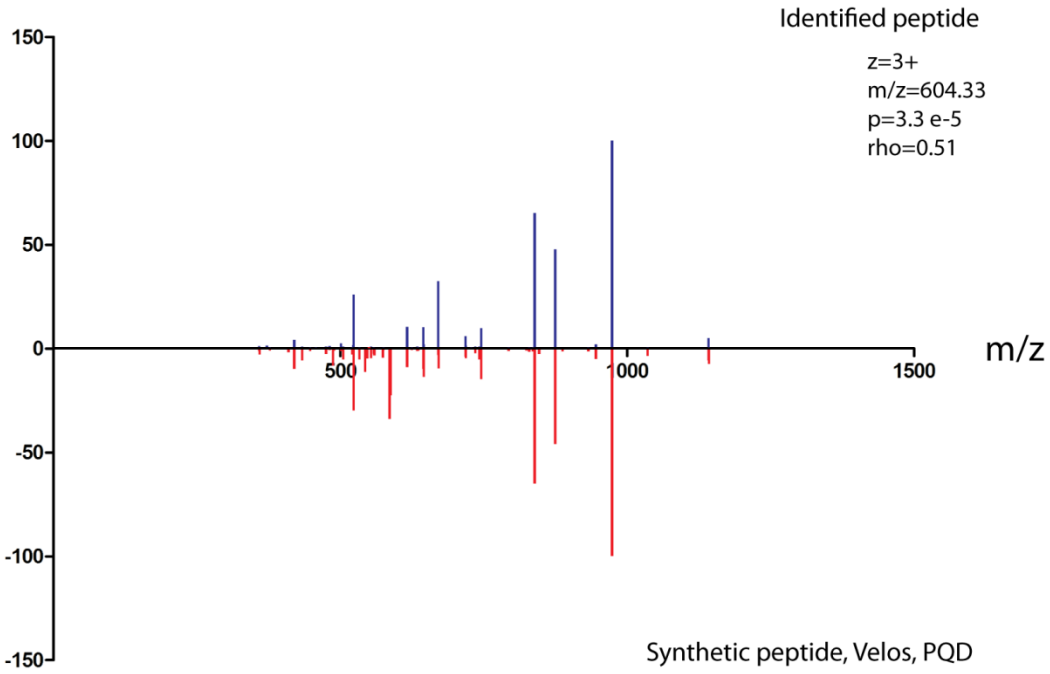
Supplementary Figure 2. Known and novel peptides mapping to Centg2 (Agap1) (A) Amino acid sequence for Centg2 (Agap1), canonical peptides that were detected covering the amino acid sequence (17%) are highlighted in yellow. The protein sequence is formatted into 10 residue blocks for readability and the location of the gap is a coincidence. The red dash indicated with double arrows show the novel exon region where the two novel peptides are identified. A canonical peptide's (VGIVGNLASGK) spectrum along with its fragmentation pattern is shown. **(B)** Validation of one of the novel peptides (AAAAGPGAASEHR) by comparing with its synthetic peptide. The matched m/z ions of the identified peptide (top) and the synthetic peptide (bottom) are shown. Spearman ranked correlation test indicates a good correlation (ρ value 0.96) with a significant p-value (1.2 e^{-22}) between the matched ions identified in the two spectra. The fragmentation table shows common ions (green), those which are observed in identified novel peptide (blue) and those which are detected in the synthetic spectra (pink). **(C)** Screenshot from the UCSC genome browser of the Centg2 (Agap1) locus for mouse where two novel peptides were identified overlapping the first intron.



Overlapped Fragmentation Table

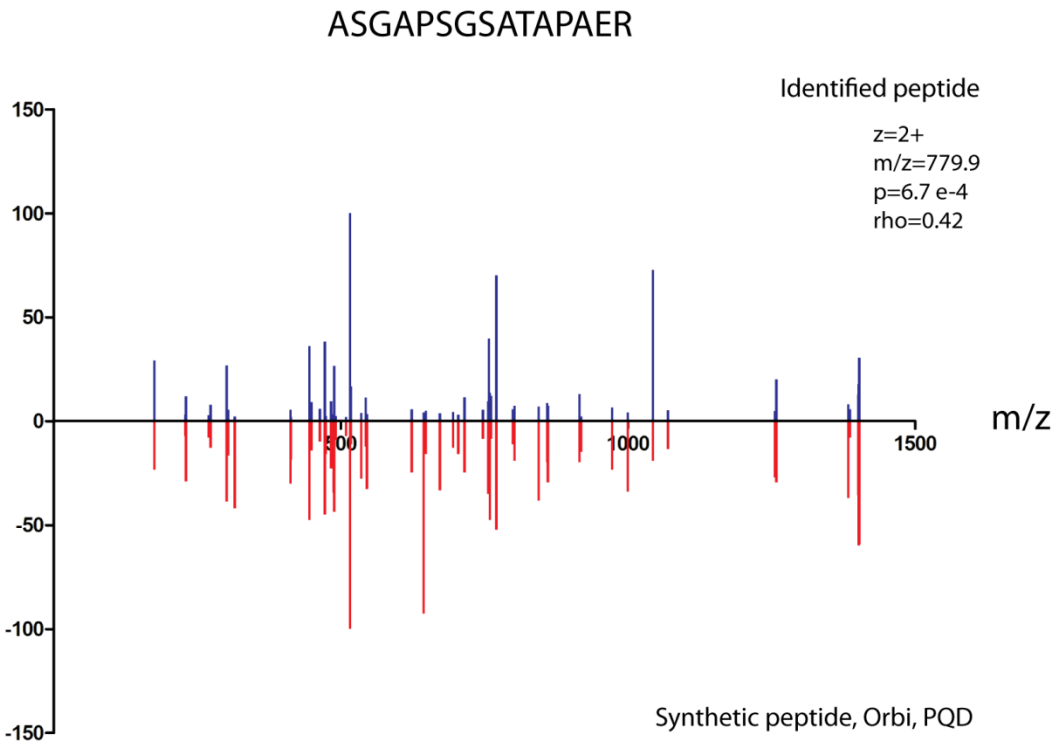
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	301.21	151.11	A+229	1,742.03	871.52	13
2	372.24	186.63	A	1,441.83	721.42	12
3	487.27	244.14	D	1,370.80	685.9	11
4	600.36	300.68	I	1,255.77	628.39	10
5	728.41	364.71	Q	1,142.68	571.85	9
6	785.44	393.22	G	1,014.63	507.82	8
7	856.47	428.74	A	957.6	479.31	7
8	943.5	472.26	S	886.57	443.79	6
9	1,056.59	528.8	L	799.54	400.27	5
10	1,113.61	557.31	G	686.45	343.73	4
11	1,210.66	605.84	P	629.43	315.22	3
12	1,366.76	683.89	R	532.38	266.69	2
13	1,742.03	871.52	K+229	376.28	188.64	1

AAEDEEVPAFFK



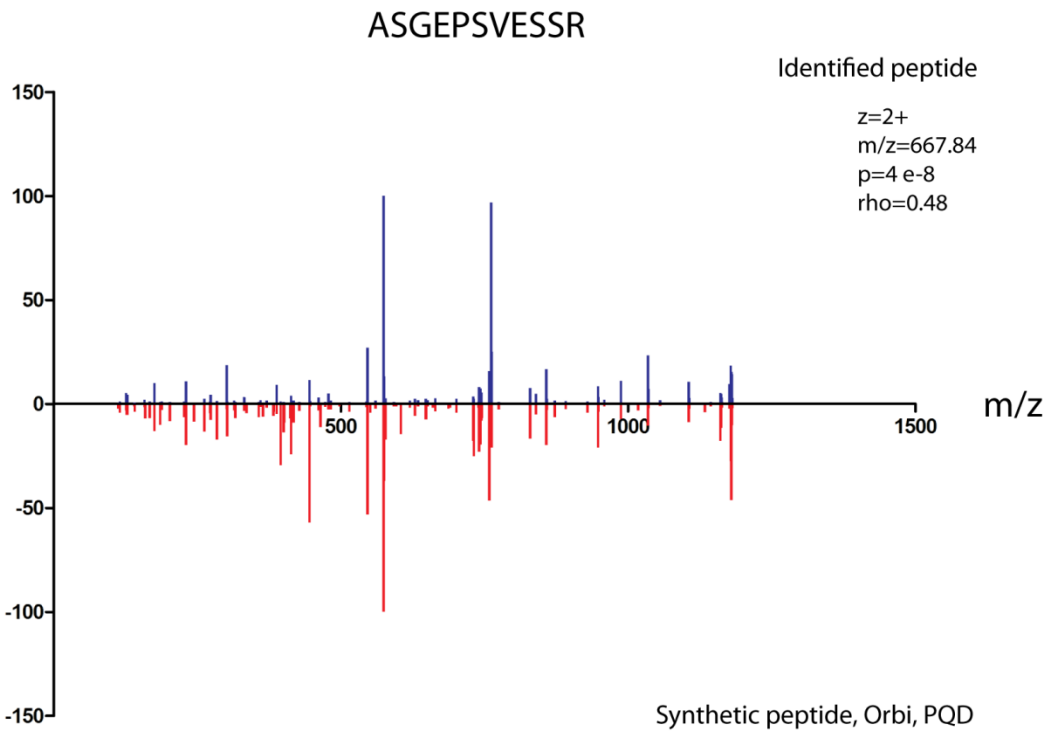
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	301.21	151.11	**A+229**	1,810.96	905.99	**12**
2	372.24	186.63	**A**	1,510.76	755.89	**11**
3	501.29	251.15	**E**	1,439.73	720.37	**10**
4	616.31	308.66	**D**	1,310.68	655.85	**9**
5	745.36	373.18	**E**	1,195.66	598.33	**8**
6	874.4	437.7	**E**	1,066.61	533.81	**7**
7	973.47	487.24	**V**	937.57	469.29	**6**
8	1,070.52	535.76	**P**	838.5	419.75	**5**
9	1,141.56	571.28	**A**	741.45	371.23	**4**
10	1,288.63	644.82	**F**	670.41	335.71	**3**
11	1,435.69	718.35	**F**	523.34	262.18	**2**
12	1,810.96	905.99	**K+229**	376.28	188.64	**1**



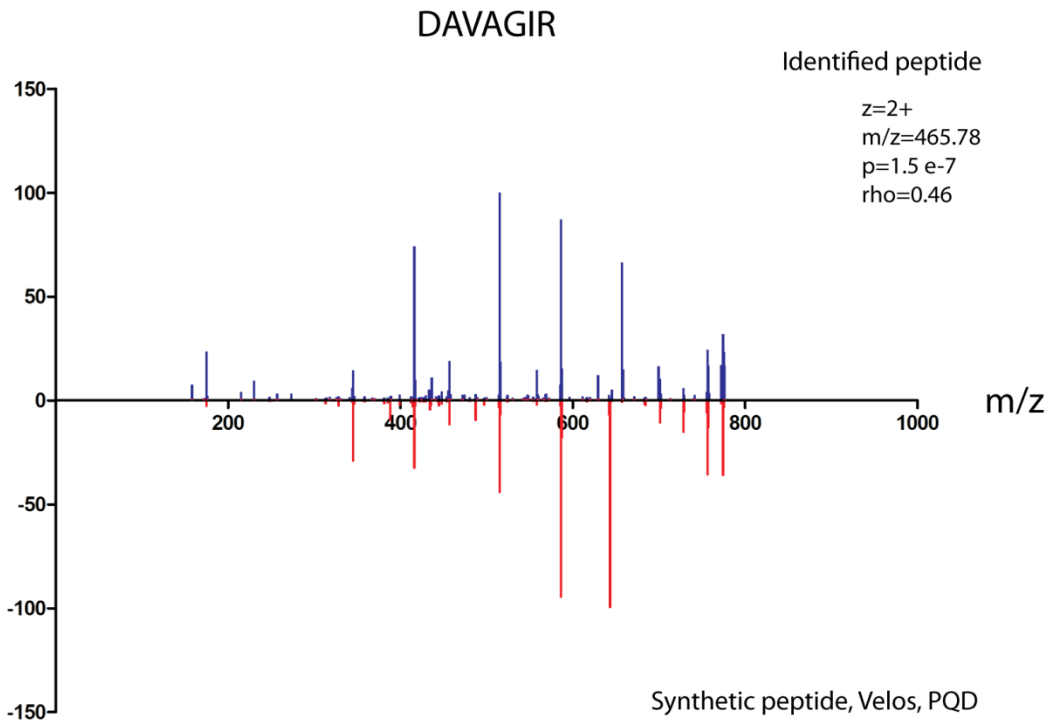
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	301.21		A+229	1,558.80	779.9	15
2	388.24		S	1,258.60	629.8	14
3	445.26		G	1,171.57	586.29	13
4	516.3		A	1,114.55	557.78	12
5	613.35		P	1,043.51	522.26	11
6	700.38	350.69	S	946.46	473.73	10
7	757.4	379.21	G	859.43	430.22	9
8	844.44	422.72	S	802.41	401.71	8
9	915.47	458.24	A	715.37	358.19	7
10	1,016.52	508.76	T	644.34	322.67	6
11	1,087.56	544.28	A	543.29		5
12	1,184.61	592.81	P	472.25		4
13	1,255.65	628.33	A	375.2		3
14	1,384.69	692.85	E	304.16		2
15	1,558.80	779.9	R	175.12		1



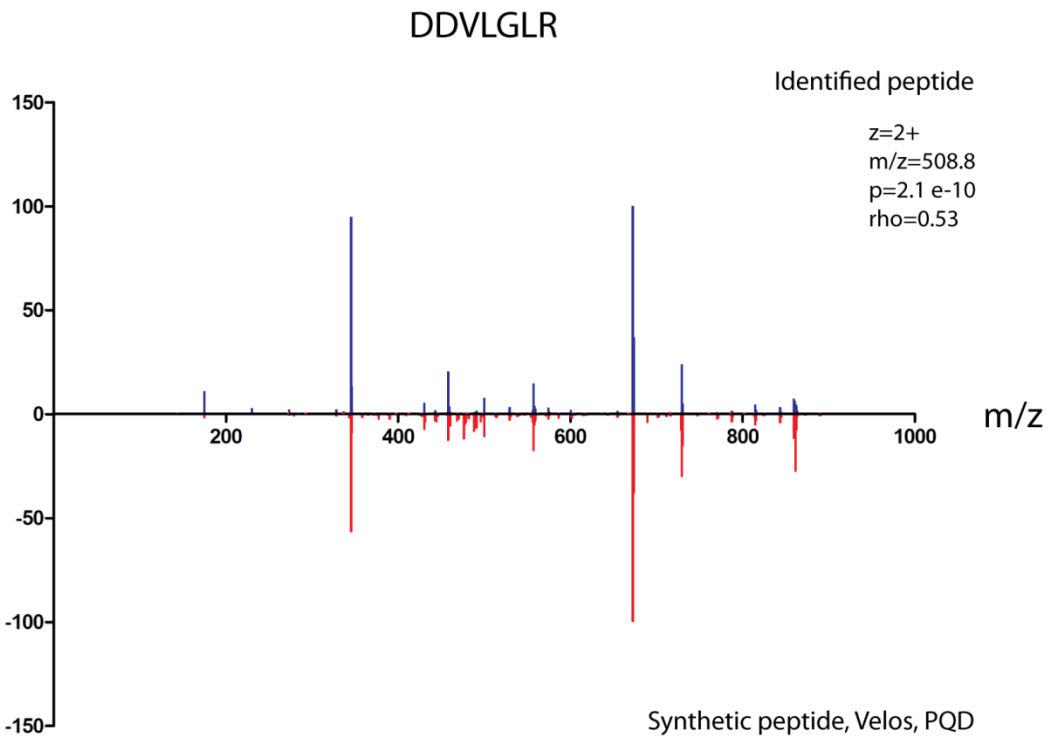
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	301.21	151.1	**A+229**	1,334.67	667.84	11
2	388.24	194.62	**S**	1,034.47	517.74	10
3	445.26	223.13	**G**	947.44	474.23	9
4	574.3	287.65	**E**	890.42	445.71	8
5	671.36	336.18	**P**	761.38	381.19	7
6	758.39	379.7	**S**	664.33	332.67	6
7	857.46	429.23	**V**	577.29	289.15	5
8	986.5	493.75	**E**	478.23	239.61	4
9	1,073.53	537.27	**S**	349.18	175.09	3
10	1,160.56	580.79	**S**	262.15	131.57	2
11	1,334.67	667.84	**R**	175.12	88.06	1



Overlapped Fragmentation Table

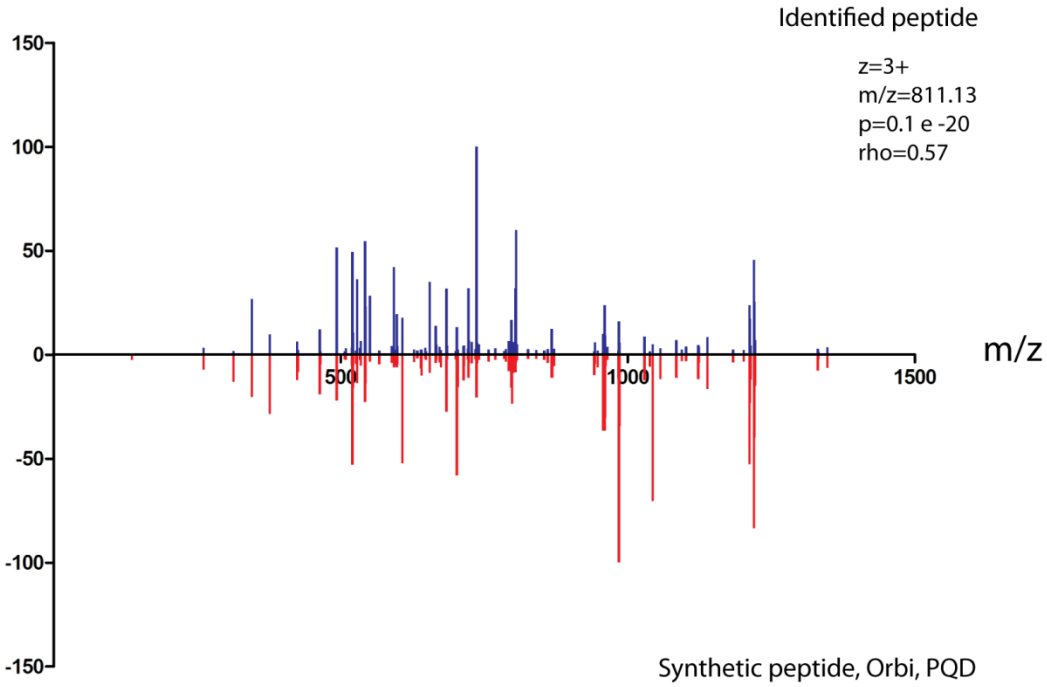
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	345.2		D+229	930.56	465.78	7
2	416.23		A	586.37	293.69	6
3	515.3		V	515.33		5
4	586.34		A	416.26		4
5	643.36		G	345.22		3
6	756.45	378.73	I	288.2		2
7	930.56	465.78	R	175.12		1



Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	345.2		D+229	1,016.59	508.8	7
2	460.22		D	672.4	336.71	6
3	559.29		V	557.38		5
4	672.38		L	458.31		4
5	729.4		G	345.22		3
6	842.48	421.74	L	288.2		2
7	1,016.59	508.8	R	175.12		1

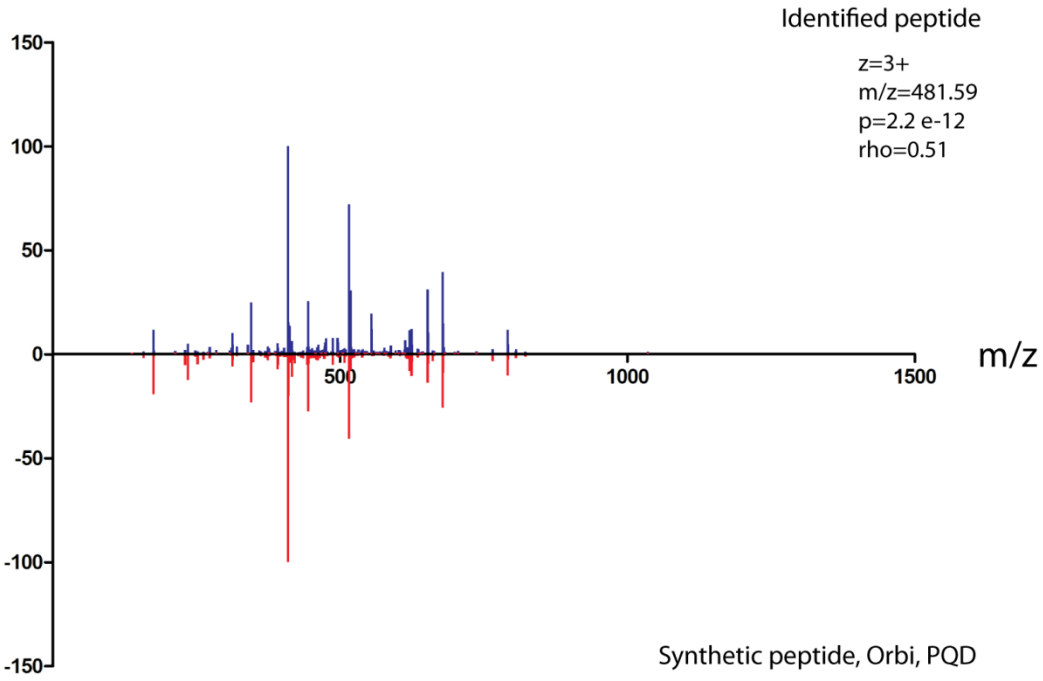
DKPANVQPYYLYGSK



Overlapped Fragmentation Table

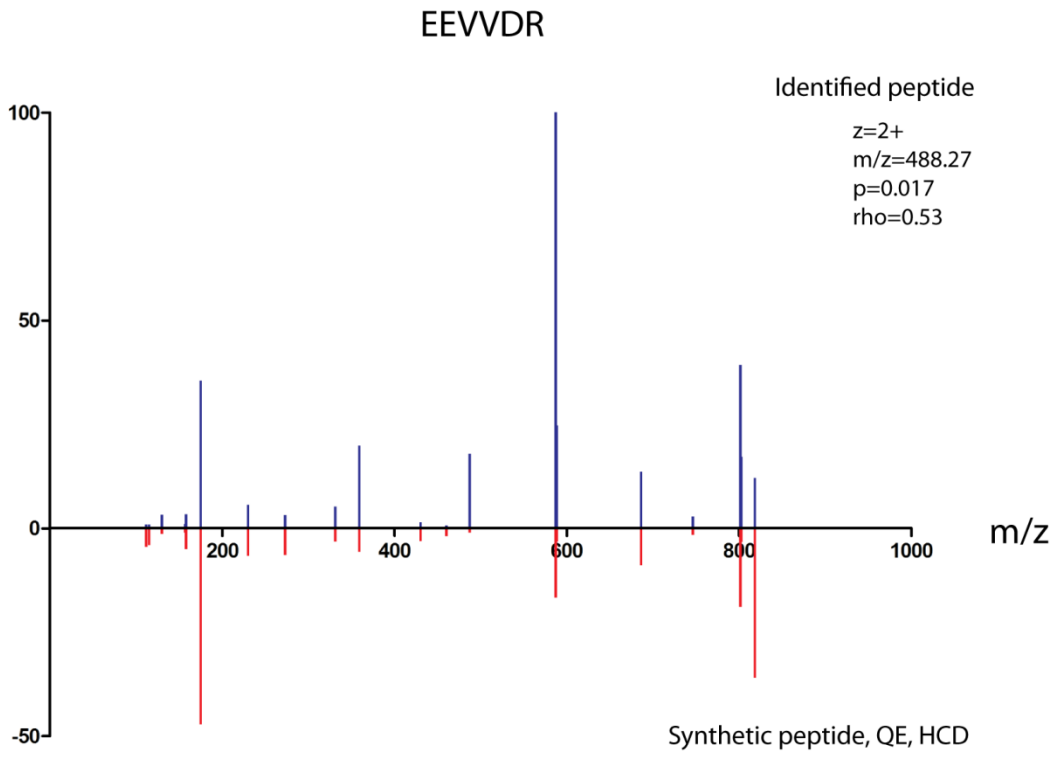
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	345.2	173.1	D+229	2,430.36	1,215.69	15
2	702.46	351.73	K+229	2,086.17	1,043.59	14
3	799.51	400.26	P	1,728.92	864.96	13
4	870.55	435.78	A	1,631.86	816.44	12
5	984.59	492.8	N	1,560.83	780.92	11
6	1,083.66	542.33	V	1,446.78	723.9	10
7	1,211.71	606.36	Q	1,347.71	674.36	9
8	1,308.77	654.89	P	1,219.66	610.33	8
9	1,471.83	736.42	Y	1,122.60	561.81	7
10	1,634.89	817.95	Y	959.54	480.27	6
11	1,747.98	874.49	L	796.48	398.74	5
12	1,911.04	956.02	Y	683.39	342.2	4
13	1,968.06	984.54	G	520.33	260.67	3
14	2,055.10	1,028.05	S	463.31	232.16	2
15	2,430.36	1,215.69	K+229	376.28	188.64	1

DVAHLGPDPHR



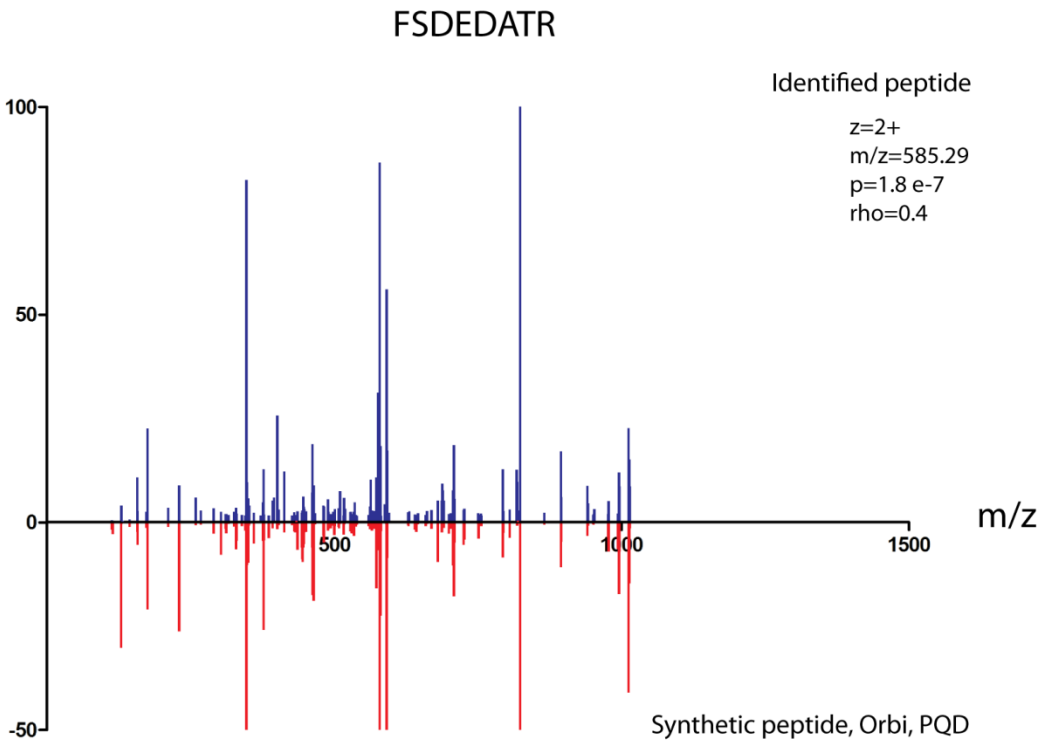
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	345.2	173.1	**D+229**	1,442.77	721.89	**11**
2	444.27	222.64	**V**	1,098.58	549.79	**10**
3	515.3	258.15	**A**	999.51	500.26	**9**
4	652.36	326.68	**H**	928.47	464.74	**8**
5	765.45	383.23	**L**	791.42	396.21	**7**
6	822.47	411.74	**G**	678.33	339.67	**6**
7	919.52	460.26	**P**	621.31	311.16	**5**
8	1,034.55	517.78	**D**	524.26	262.63	**4**
9	1,131.60	566.3	**P**	409.23	205.12	**3**
10	1,268.66	634.83	**H**	312.18	156.59	**2**
11	1,442.77	721.89	**R**	175.12	88.06	**1**



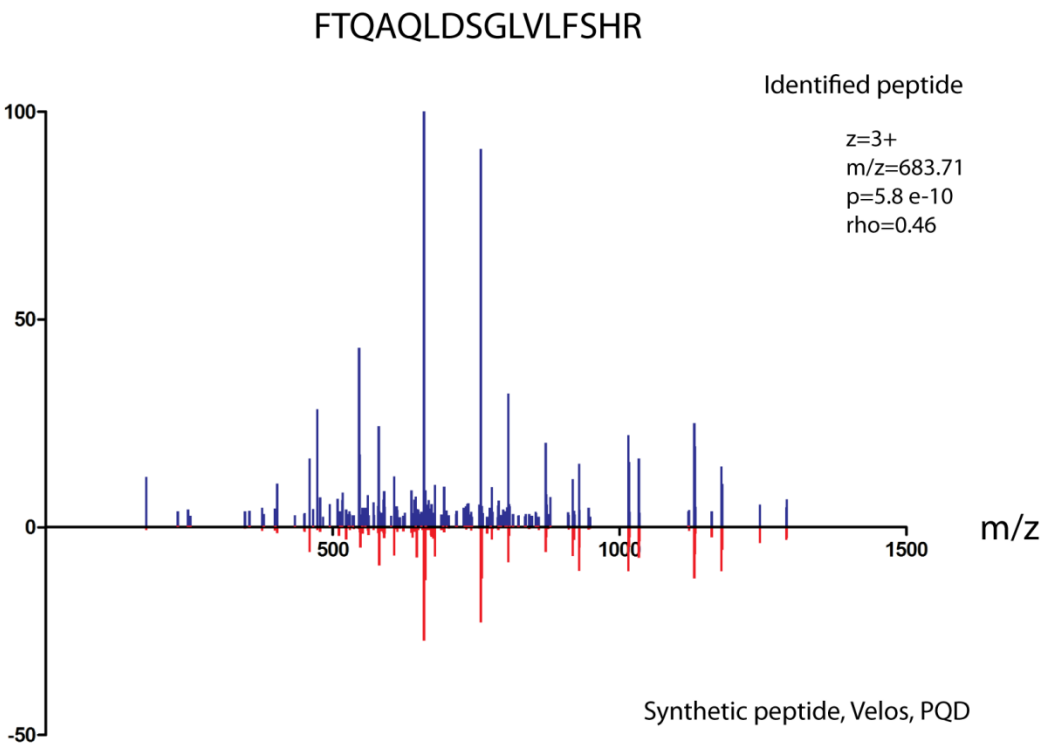
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	359.21		E+229	975.53	488.27	6
2	488.26		E	617.33		5
3	587.32		V	488.28		4
4	686.39		V	389.21		3
5	801.42		D	290.15		2
6	975.53	488.27	R	175.12		1



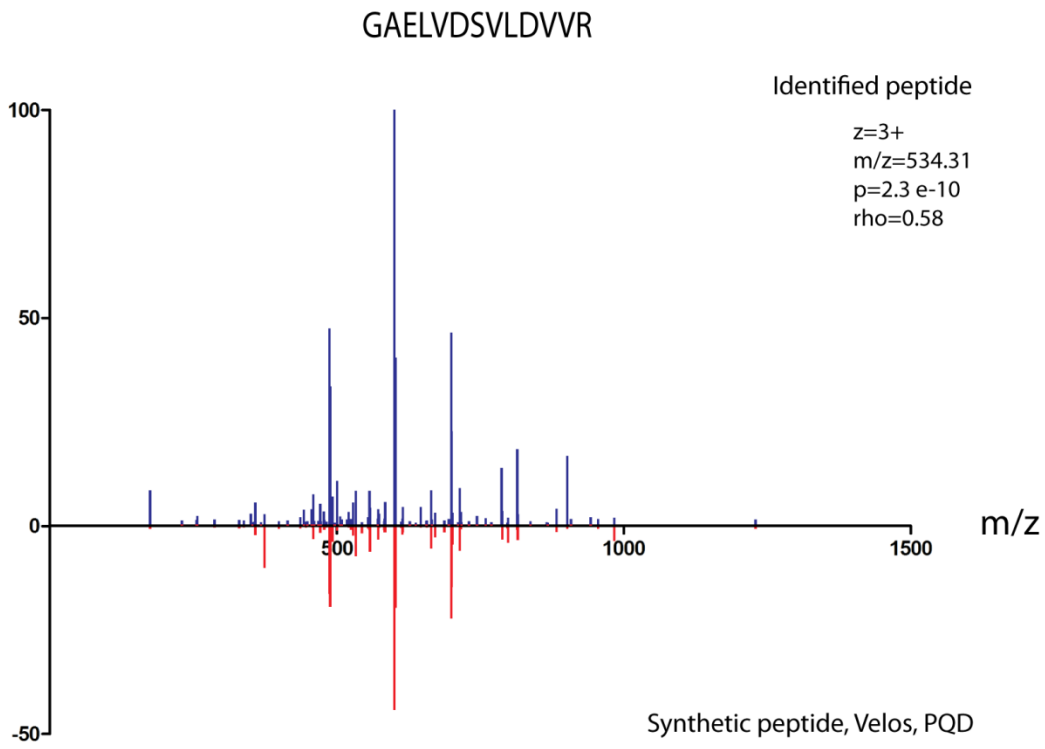
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	377.24		F+229	1,169.56	585.29	8
2	464.27		S	793.33	397.17	7
3	579.3		D	706.3	353.65	6
4	708.34		E	591.27		5
5	823.37		D	462.23		4
6	894.4	447.71	A	347.2		3
7	995.45	498.23	T	276.17		2
8	1,169.56	585.29	R	175.12		1



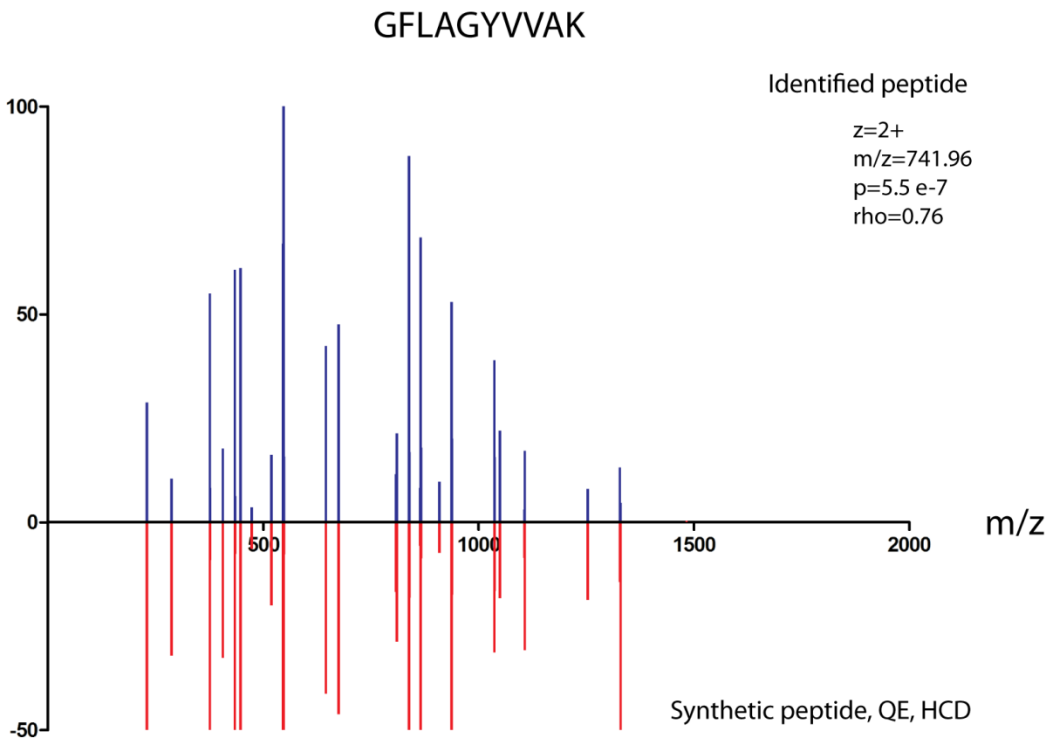
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	377.24	189.12	F+229	2,048.11	1,024.56	16
2	478.29	239.65	T	1,671.88	836.44	15
3	606.34	303.68	Q	1,570.83	785.92	14
4	677.38	339.19	A	1,442.78	721.89	13
5	805.44	403.22	Q	1,371.74	686.37	12
6	918.52	459.77	L	1,243.68	622.34	11
7	1,033.55	517.28	D	1,130.60	565.8	10
8	1,120.58	560.8	S	1,015.57	508.29	9
9	1,177.61	589.31	G	928.54	464.77	8
10	1,290.69	645.85	L	871.51	436.26	7
11	1,389.76	695.38	V	758.43	379.72	6
12	1,502.84	751.92	L	659.36	330.18	5
13	1,649.91	825.46	F	546.28	273.64	4
14	1,736.94	868.97	S	399.21	200.11	3
15	1,874.00	937.5	H	312.18	156.59	2
16	2,048.11	1,024.56	R	175.12	88.06	1



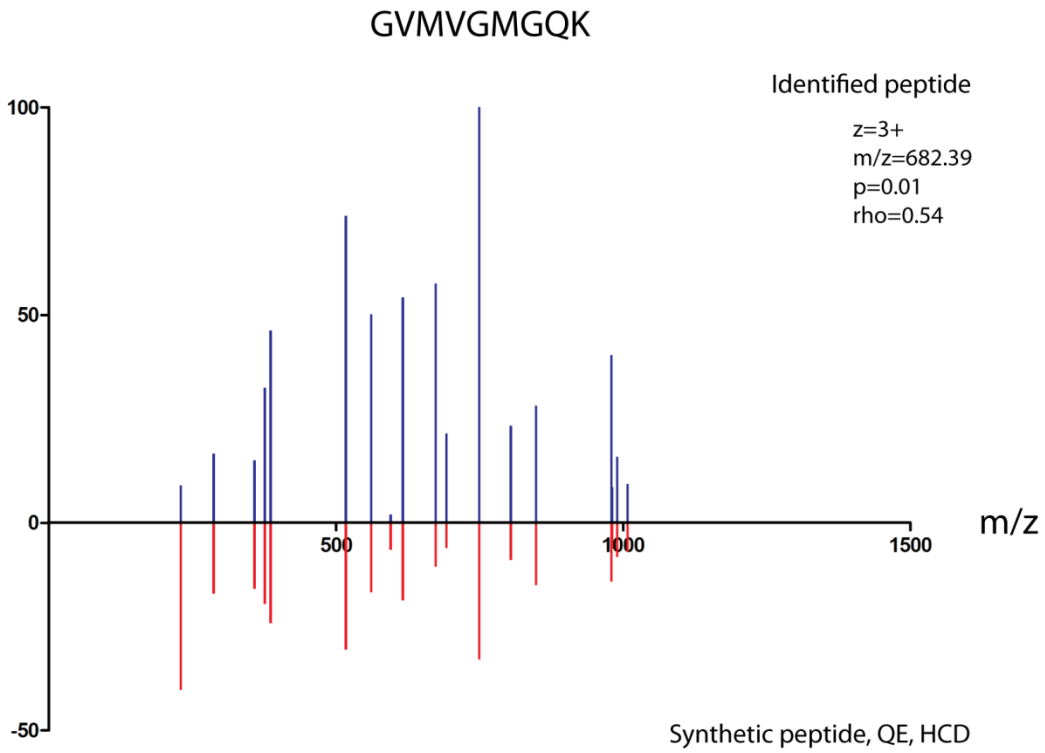
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	287.19	144.1	**G+229**	1,600.91	800.96	**13**
2	358.23	179.62	**A**	1,314.73	657.87	**12**
3	487.27	244.14	**E**	1,243.69	622.35	**11**
4	600.36	300.68	**L**	1,114.65	557.83	**10**
5	699.42	350.22	**V**	1,001.56	501.28	**9**
6	814.45	407.73	**D**	902.49	451.75	**8**
7	901.48	451.25	**S**	787.47	394.24	**7**
8	1,000.55	500.78	**V**	700.44	350.72	**6**
9	1,113.64	557.32	**L**	601.37	301.19	**5**
10	1,228.66	614.83	**D**	488.28	244.65	**4**
11	1,327.73	664.37	**V**	373.26	187.13	**3**
12	1,426.80	713.9	**V**	274.19	137.6	**2**
13	1,600.91	800.96	**R**	175.12	88.06	**1**



Overlapped Fragmentation Table

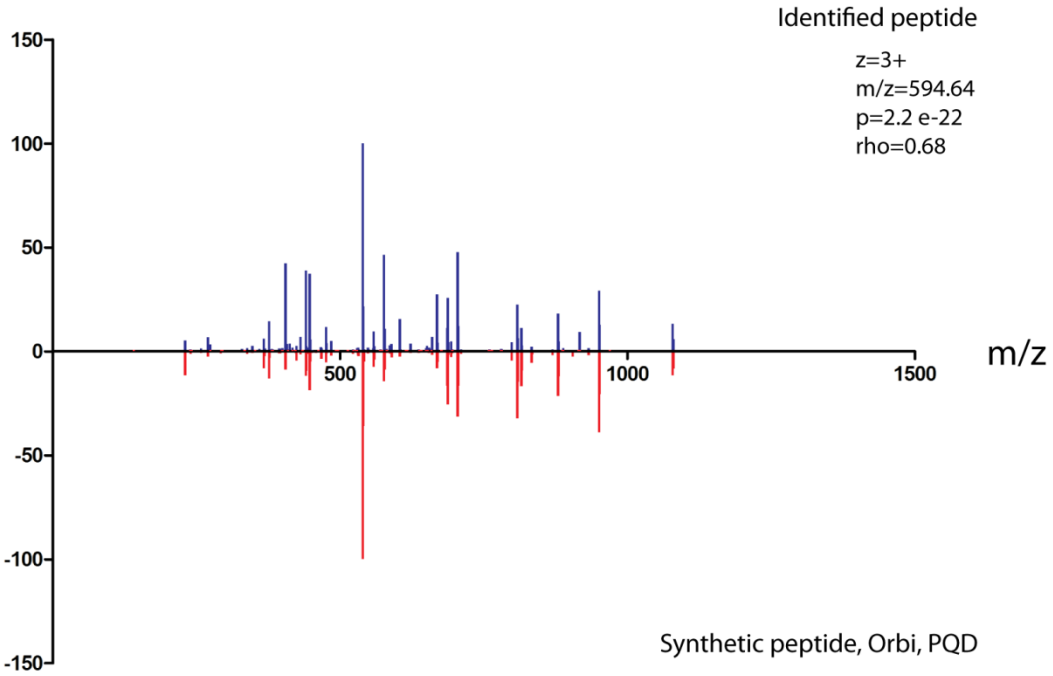
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	287.19		**G+229**	1,482.91	741.96	**10**
2	434.26		**F**	1,196.72	598.87	**9**
3	547.34		**L**	1,049.66	525.33	**8**
4	618.38		**A**	936.57	468.79	**7**
5	675.4		**G**	865.53	433.27	**6**
6	838.47	419.74	**Y**	808.51		**5**
7	937.53	469.27	**V**	645.45		**4**
8	1,036.60	518.81	**V**	546.38		**3**
9	1,107.64	554.32	**A**	447.31		**2**
10	1,482.91	741.96	**K+229**	376.28		**1**



Overlapped Fragmentation Table

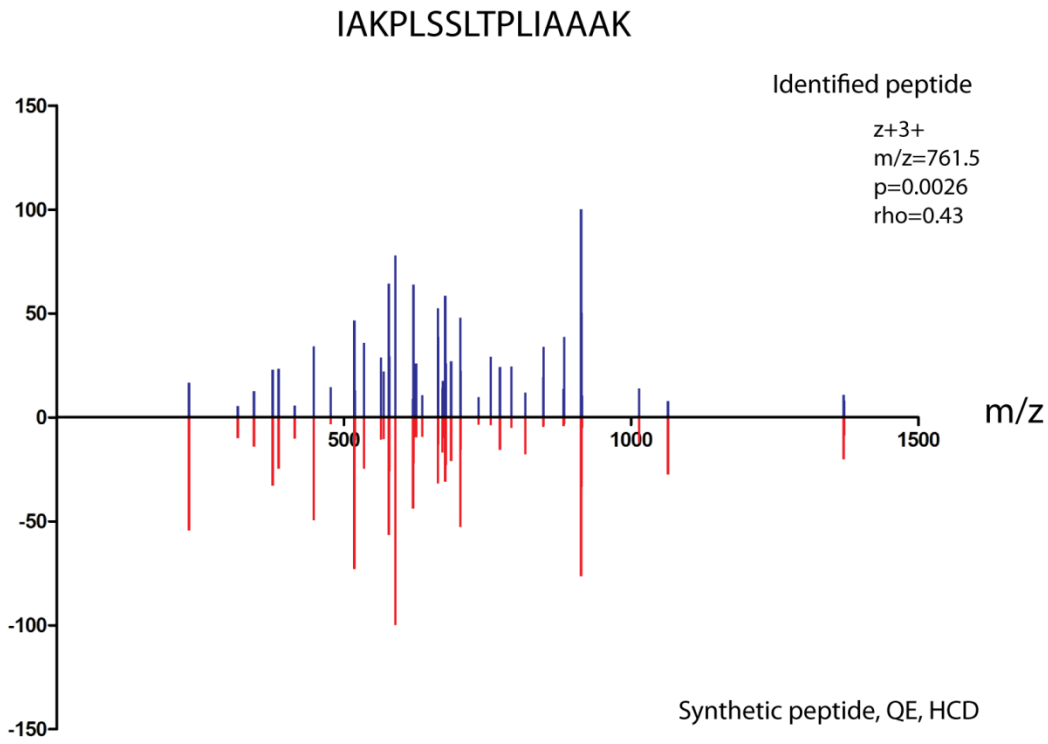
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	287.19		G+229	1,364.78	682.89	9
2	386.26		V	1,078.60	539.8	8
3	517.3		M	979.53	490.27	7
4	616.37		V	848.49	424.75	6
5	673.39		G	749.42		5
6	804.43	402.72	M	692.4		4
7	861.45	431.23	G	561.36		3
8	989.51	495.26	Q	504.33		2
9	1,364.78	682.89	K+229	376.28		1

HGDPGDAAQQEAK



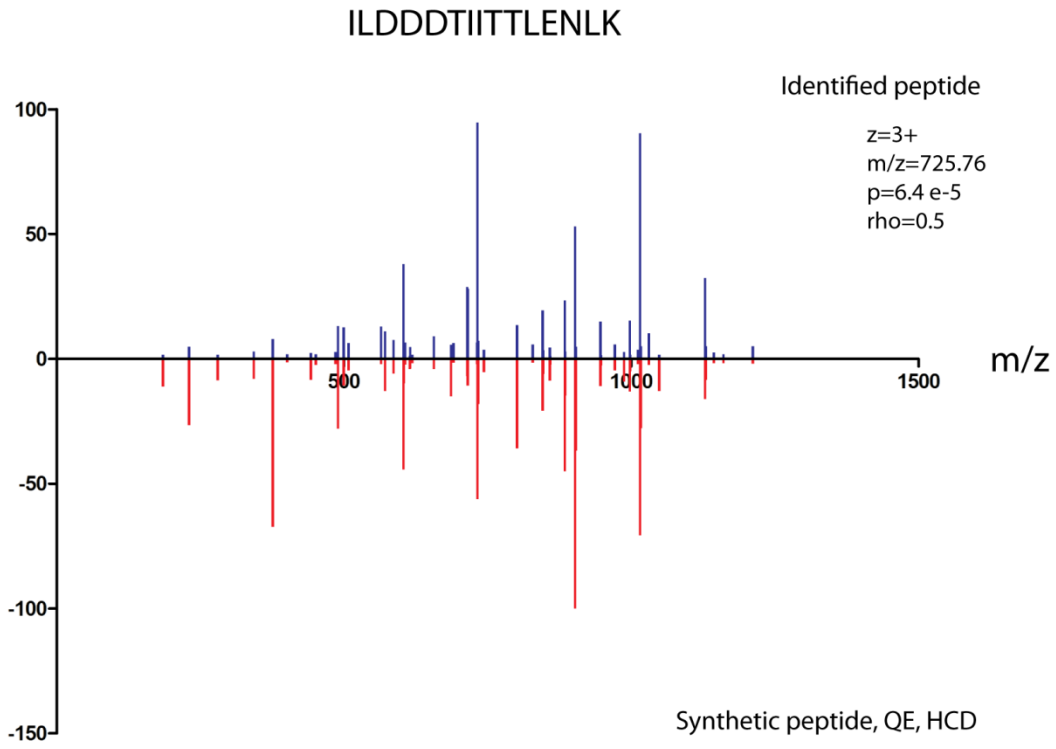
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	367.23	184.12	H+229	1,781.92	891.46	13
2	424.25	212.63	G	1,415.70	708.35	12
3	539.28	270.14	D	1,358.68	679.84	11
4	636.33	318.67	P	1,243.65	622.33	10
5	693.35	347.18	G	1,146.60	573.8	9
6	808.38	404.69	D	1,089.57	545.29	8
7	879.42	440.21	A	974.55	487.78	7
8	950.45	475.73	A	903.51	452.26	6
9	1,078.51	539.76	Q	832.47	416.74	5
10	1,206.57	603.79	Q	704.41	352.71	4
11	1,335.61	668.31	E	576.36	288.68	3
12	1,406.65	703.83	A	447.31	224.16	2
13	1,781.92	891.46	K+229	376.28	188.64	1



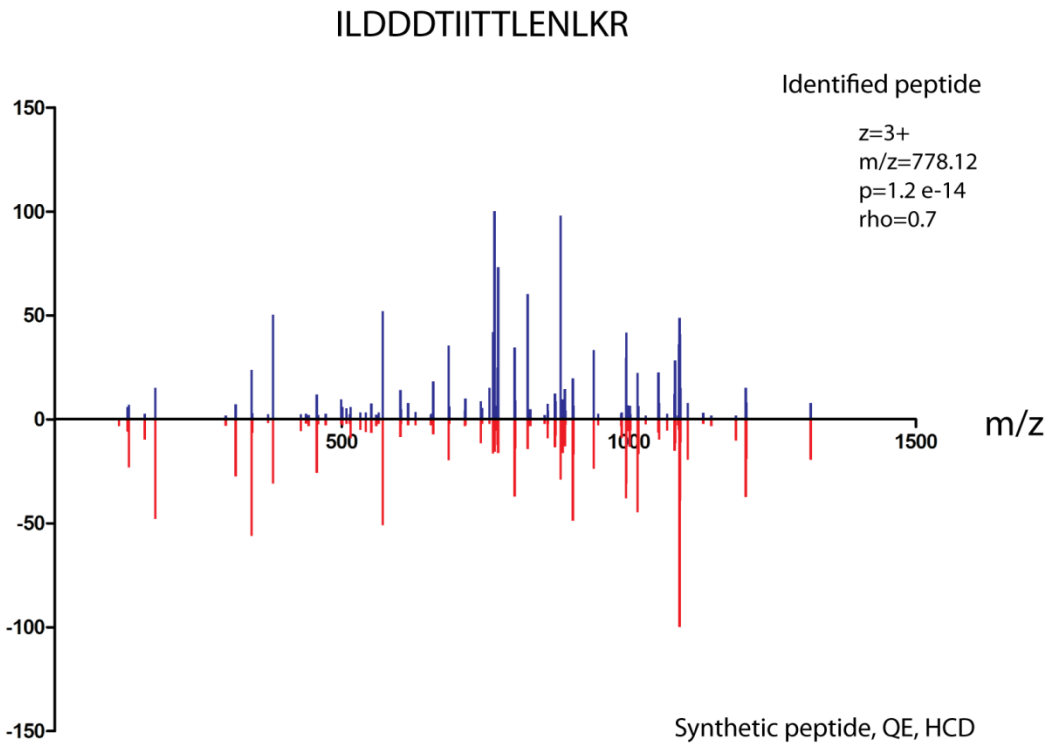
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25	172.13	**I+229**	2,281.48	1,141.25	**16**
2	414.29	207.65	**A**	1,939.24	970.12	**15**
3	771.55	386.28	**K+229**	1,868.20	934.6	**14**
4	868.6	434.8	**P**	1,510.94	755.97	**13**
5	981.69	491.35	**L**	1,413.89	707.45	**12**
6	1,068.72	534.86	**S**	1,300.80	650.91	**11**
7	1,155.75	578.38	**S**	1,213.77	607.39	**10**
8	1,268.83	634.92	**L**	1,126.74	563.87	**9**
9	1,369.88	685.44	**T**	1,013.66	507.33	**8**
10	1,466.93	733.97	**P**	912.61	456.81	**7**
11	1,580.02	790.51	**L**	815.56	408.28	**6**
12	1,693.10	847.06	**I**	702.47	351.74	**5**
13	1,764.14	882.57	**A**	589.39	295.2	**4**
14	1,835.18	918.09	**A**	518.35	259.68	**3**
15	1,906.21	953.61	**A**	447.31	224.16	**2**
16	2,281.48	1,141.25	**K+229**	376.28	188.64	**1**



Overlapped Fragmentation Table

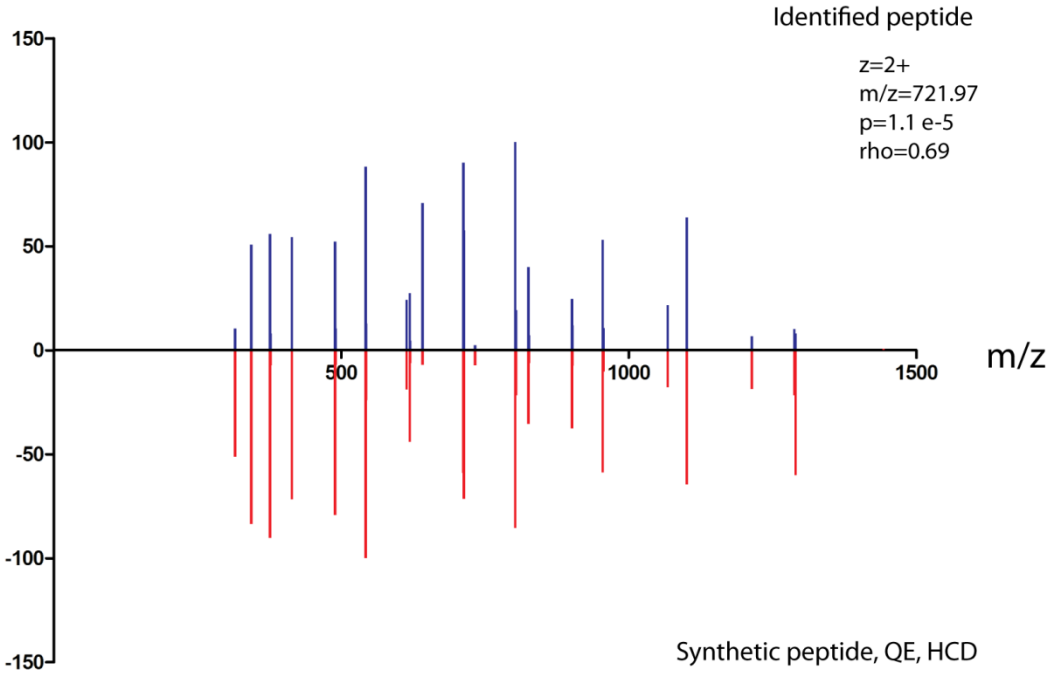
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25	172.13	**I+229**	2,175.25	1,088.13	**15**
2	456.34	228.67	**L**	1,833.01	917.01	**14**
3	571.37	286.19	**D**	1,719.92	860.46	**13**
4	686.39	343.7	**D**	1,604.89	802.95	**12**
5	801.42	401.21	**D**	1,489.87	745.44	**11**
6	902.47	451.74	**T**	1,374.84	687.92	**10**
7	1,015.55	508.28	**I**	1,273.79	637.4	**9**
8	1,128.64	564.82	**I**	1,160.71	580.86	**8**
9	1,229.68	615.35	**T**	1,047.62	524.32	**7**
10	1,330.73	665.87	**T**	946.58	473.79	**6**
11	1,443.81	722.41	**L**	845.53	423.27	**5**
12	1,572.86	786.93	**E**	732.45	366.73	**4**
13	1,686.90	843.95	**N**	603.4	302.21	**3**
14	1,799.98	900.5	**L**	489.36	245.18	**2**
15	2,175.25	1,088.13	**K+229**	376.28	188.64	**1**



Overlapped Fragmentation Table

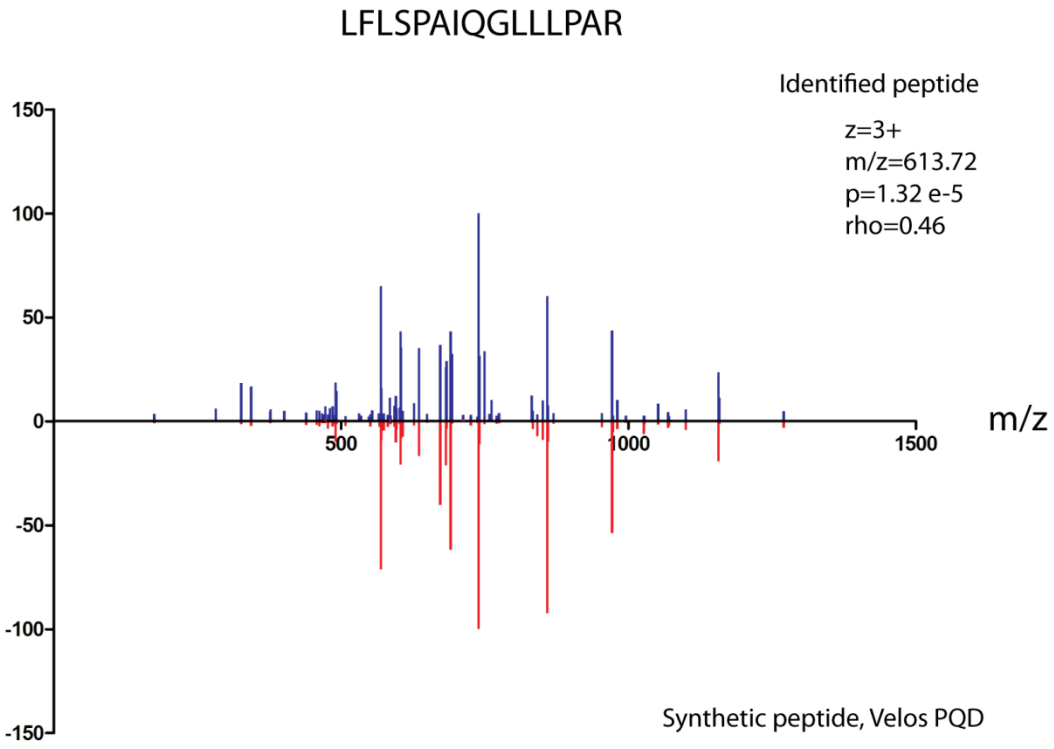
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25	172.13	**I+229**	2,331.35	1,166.18	**16**
2	456.34	228.67	**L**	1,989.11	995.06	**15**
3	571.37	286.19	**D**	1,876.02	938.52	**14**
4	686.39	343.7	**D**	1,761.00	881	**13**
5	801.42	401.21	**D**	1,645.97	823.49	**12**
6	902.47	451.74	**T**	1,530.94	765.97	**11**
7	1,015.55	508.28	**I**	1,429.89	715.45	**10**
8	1,128.64	564.82	**I**	1,316.81	658.91	**9**
9	1,229.68	615.35	**T**	1,203.73	602.37	**8**
10	1,330.73	665.87	**T**	1,102.68	551.84	**7**
11	1,443.81	722.41	**L**	1,001.63	501.32	**6**
12	1,572.86	786.93	**E**	888.55	444.78	**5**
13	1,686.90	843.95	**N**	759.5	380.26	**4**
14	1,799.98	900.5	**L**	645.46	323.23	**3**
15	2,157.24	1,079.12	**K+229**	532.38	266.69	**2**
16	2,331.35	1,166.18	**R**	175.12	88.06	**1**

LAQVALELK



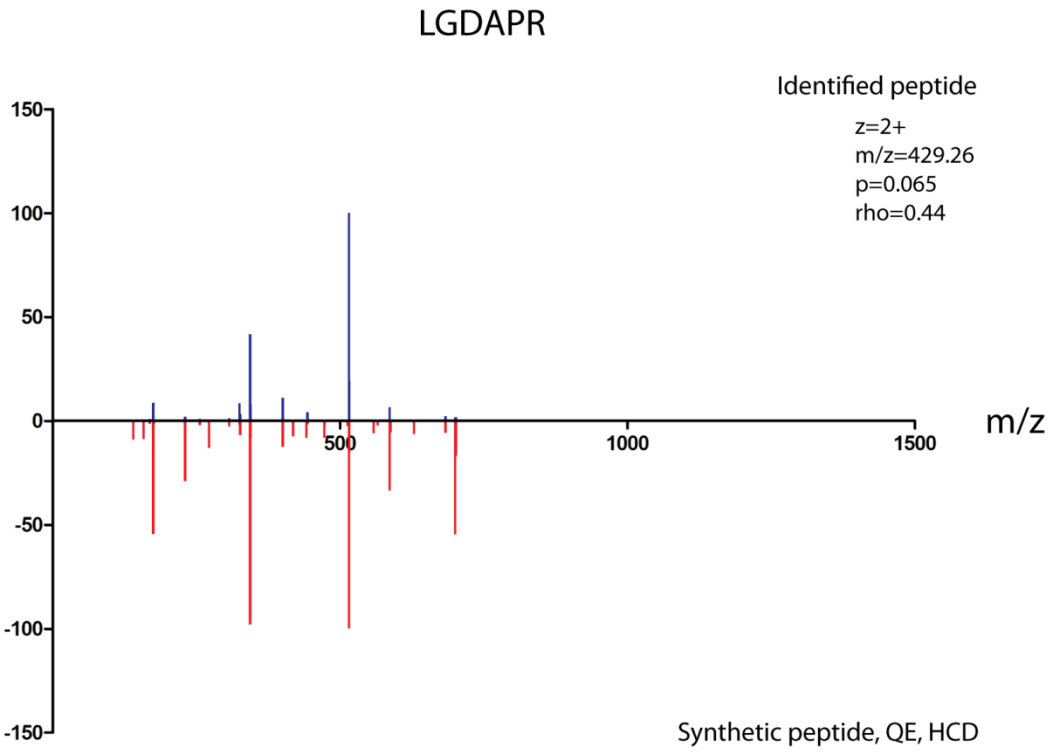
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25		L+229	1,442.93	721.97	9
2	414.29		A	1,100.69	550.85	8
3	542.35		Q	1,029.65	515.33	7
4	641.42		V	901.59	451.3	6
5	712.46		A	802.52		5
6	825.54	413.27	L	731.49		4
7	954.58	477.79	E	618.4		3
8	1,067.67	534.34	L	489.36		2
9	1,442.93	721.97	K+229	376.28		1



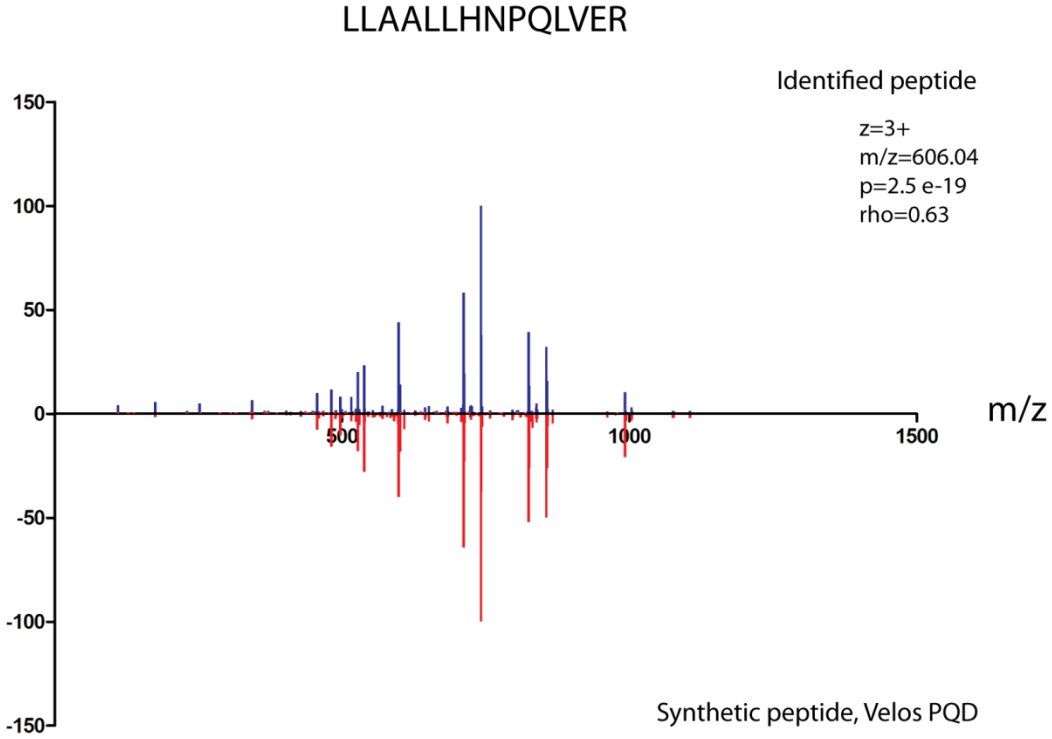
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25	172.13	**L+229**	1,838.15	919.58	**15**
2	490.32	245.66	**F**	1,495.90	748.45	**14**
3	603.41	302.21	**L**	1,348.83	674.92	**13**
4	690.44	345.72	**S**	1,235.75	618.38	**12**
5	787.49	394.25	**P**	1,148.72	574.86	**11**
6	858.53	429.77	**A**	1,051.66	526.33	**10**
7	971.61	486.31	**I**	980.63	490.82	**9**
8	1,099.67	550.34	**Q**	867.54	434.27	**8**
9	1,156.69	578.85	**G**	739.48	370.24	**7**
10	1,269.78	635.39	**L**	682.46	341.73	**6**
11	1,382.86	691.93	**L**	569.38	285.19	**5**
12	1,495.95	748.48	**L**	456.29	228.65	**4**
13	1,593.00	797	**P**	343.21	172.11	**3**
14	1,664.04	832.52	**A**	246.16	123.58	**2**
15	1,838.15	919.58	**R**	175.12	88.06	**1**



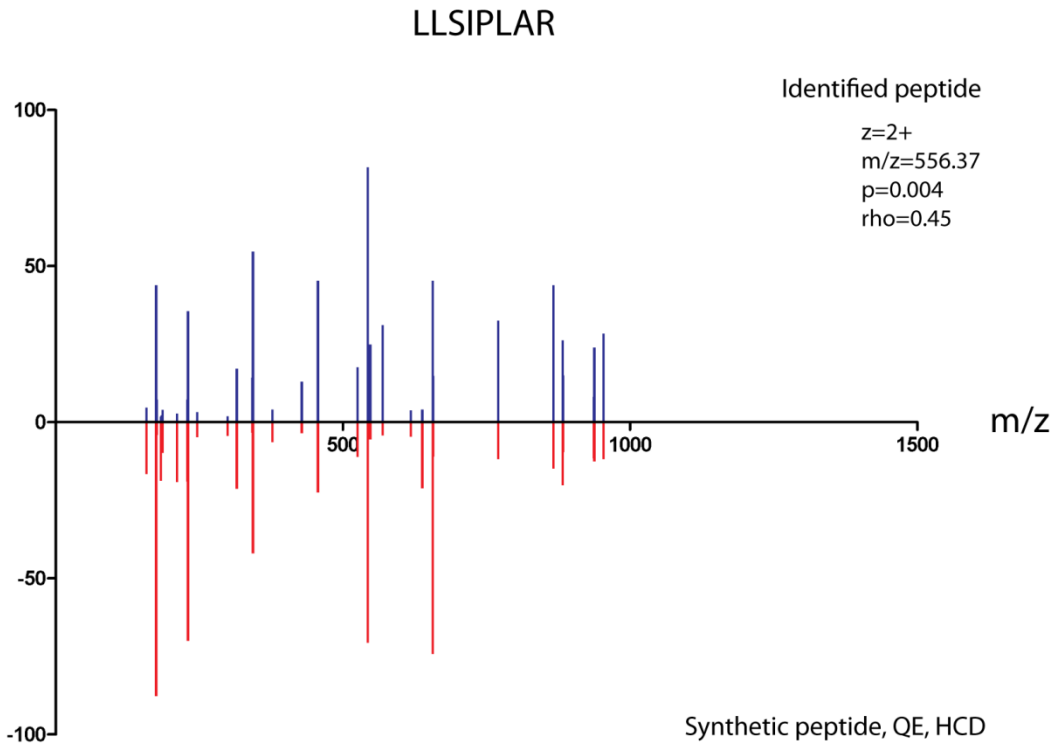
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25		L+229	857.5	429.26	6
2	400.28		G	515.26		5
3	515.3		D	458.24		4
4	586.34		A	343.21		3
5	683.39		P	272.17		2
6	857.5	429.26	R	175.12		1



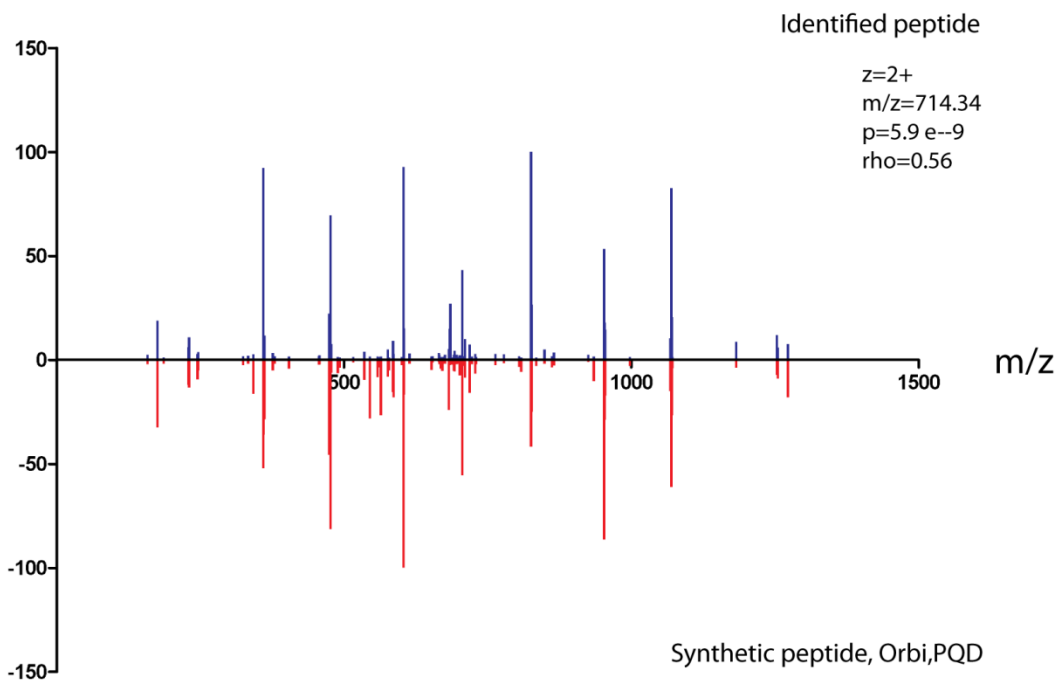
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25	172.13	**L+229**	1,816.10	908.55	**14**
2	456.34	228.67	**L**	1,473.85	737.43	**13**
3	527.38	264.19	**A**	1,360.77	680.89	**12**
4	598.41	299.71	**A**	1,289.73	645.37	**11**
5	711.5	356.25	**L**	1,218.70	609.85	**10**
6	824.58	412.79	**L**	1,105.61	553.31	**9**
7	961.64	481.32	**H**	992.53	496.77	**8**
8	1,075.68	538.34	**N**	855.47	428.24	**7**
9	1,172.74	586.87	**P**	741.43	371.22	**6**
10	1,300.79	650.9	**Q**	644.37	322.69	**5**
11	1,413.88	707.44	**L**	516.31	258.66	**4**
12	1,512.95	756.98	**V**	403.23	202.12	**3**
13	1,641.99	821.5	**E**	304.16	152.58	**2**
14	1,816.10	908.55	**R**	175.12	88.06	**1**



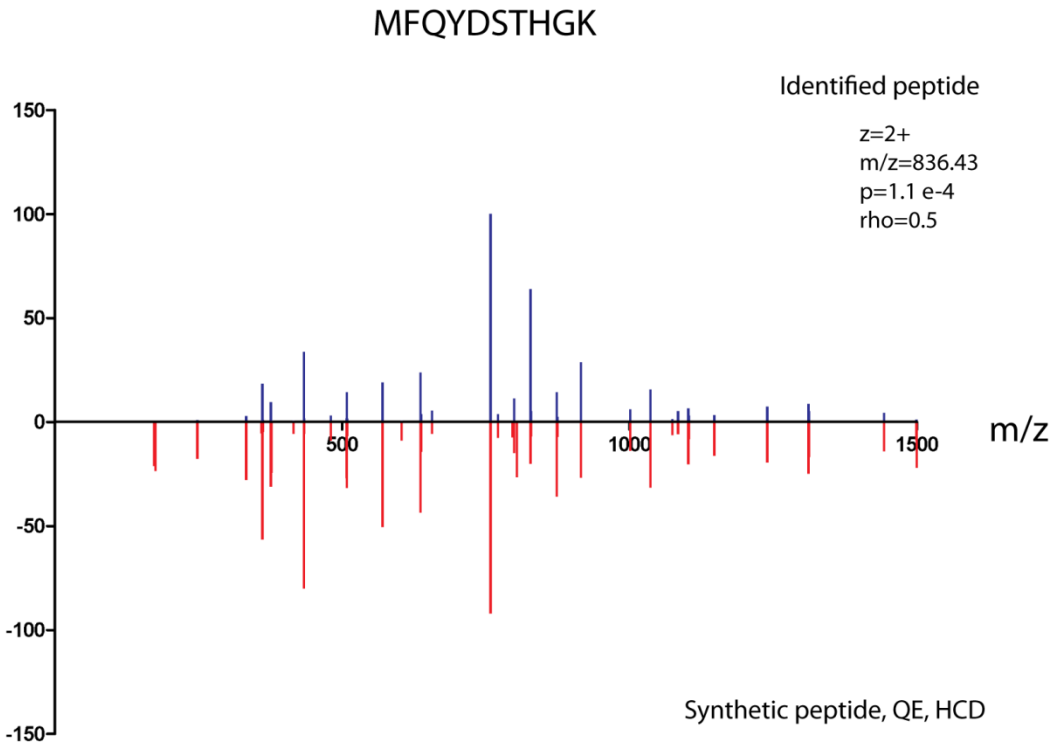
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25		**L+229**	1,111.74	556.37	**8**
2	456.34		**L**	769.49	385.25	**7**
3	543.37		**S**	656.41	328.71	**6**
4	656.45		**L**	569.38		**5**
5	769.54		**I**	456.29		**4**
6	866.59	433.8	**P**	343.21		**3**
7	937.63	469.32	**A**	246.16		**2**
8	1,111.74	556.37	**R**	175.12		**1**



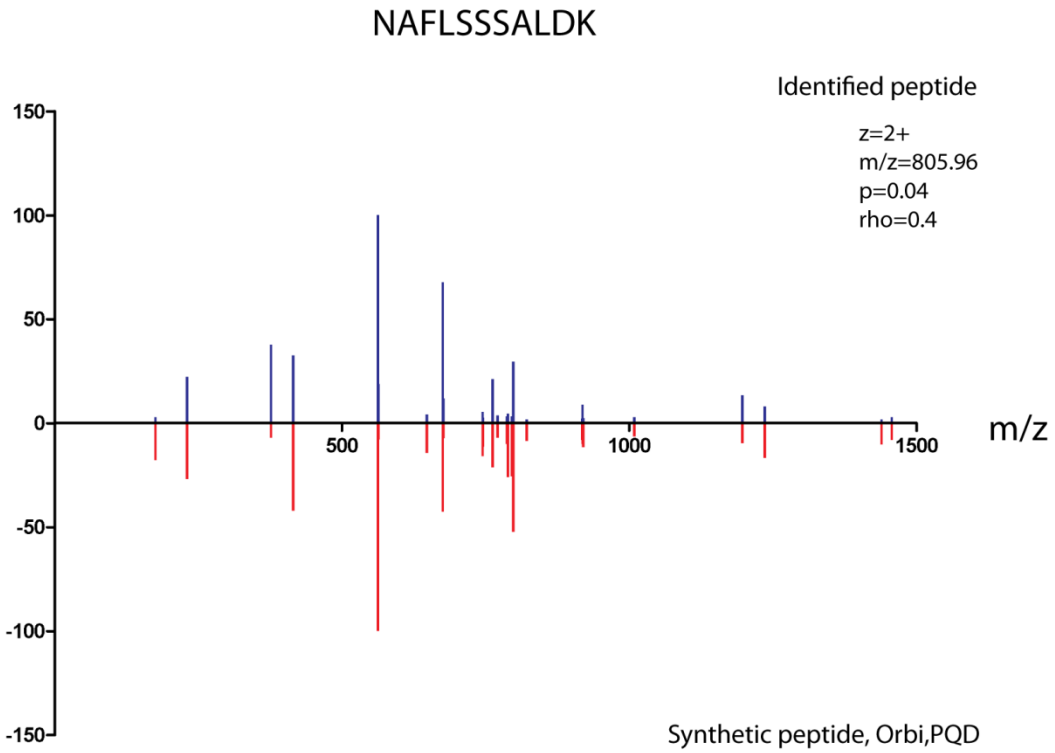
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	361.21		M+229	1,427.67	714.34	10
2	476.24		D	1,067.46	534.24	9
3	563.27		S	952.44	476.72	8
4	710.34		F	865.41	433.21	7
5	825.37		D	718.34	359.67	6
6	954.41	477.71	E	603.31	302.15	5
7	1,069.43	535.22	D	474.27	237.63	4
8	1,182.52	591.76	L	359.24	180.12	3
9	1,253.56	627.28	A	246.16		2
10	1,427.67	714.34	R	175.12		1



Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	361.21		**M+229**	1,671.86	836.43	**10**
2	508.28		**F**	1,311.65	656.33	**9**
3	636.34		**Q**	1,164.58	582.8	**8**
4	799.4		**Y**	1,036.53	518.77	**7**
5	914.43		**D**	873.46	437.24	**6**
6	1,001.46	501.23	**S**	758.44	379.72	**5**
7	1,102.51	551.76	**T**	671.4	336.21	**4**
8	1,239.57	620.29	**H**	570.36	285.68	**3**
9	1,296.59	648.8	**G**	433.3		**2**
10	1,671.86	836.43	**K+229**	376.28		**1**



Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	344.21		**N+229**	1,610.92	805.96	**11**
2	415.25		**A**	1,267.71	634.36	**10**
3	562.32		**F**	1,196.67	598.84	**9**
4	675.4		**L**	1,049.60	525.31	**8**
5	762.43		**S**	936.52	468.76	**7**
6	849.47	425.24	**S**	849.49	425.25	**6**
7	936.5	468.75	**S**	762.46		**5**
8	1,007.54	504.27	**A**	675.42		**4**
9	1,120.62	560.81	**L**	604.39		**3**
10	1,235.65	618.33	**D**	491.3		**2**
11	1,610.92	805.96	**K+229**	376.28		**1**

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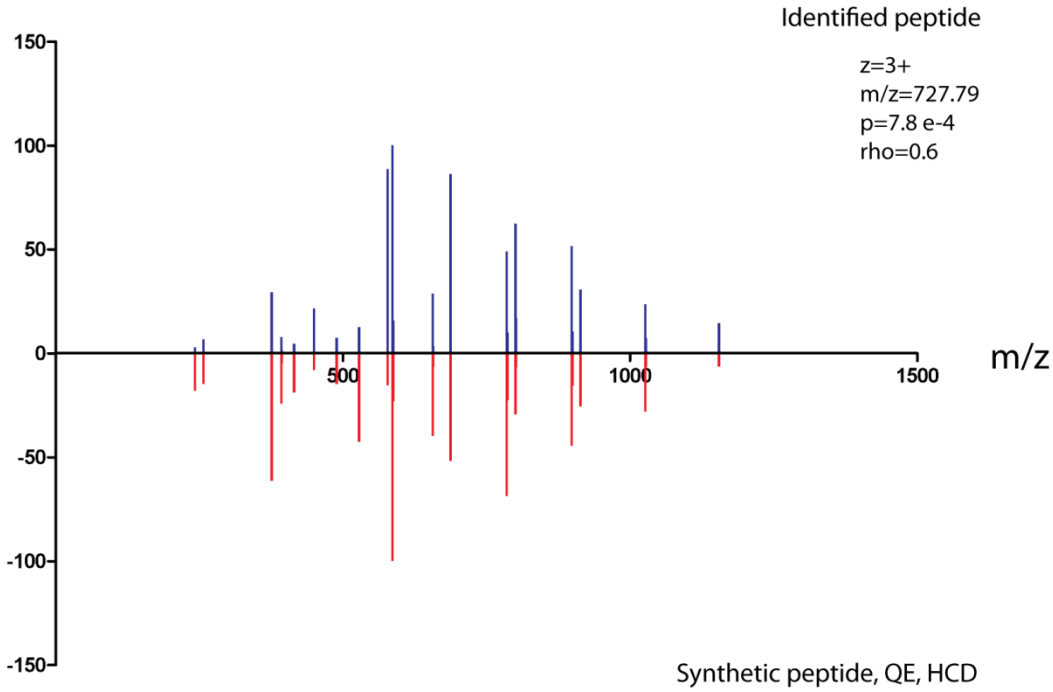
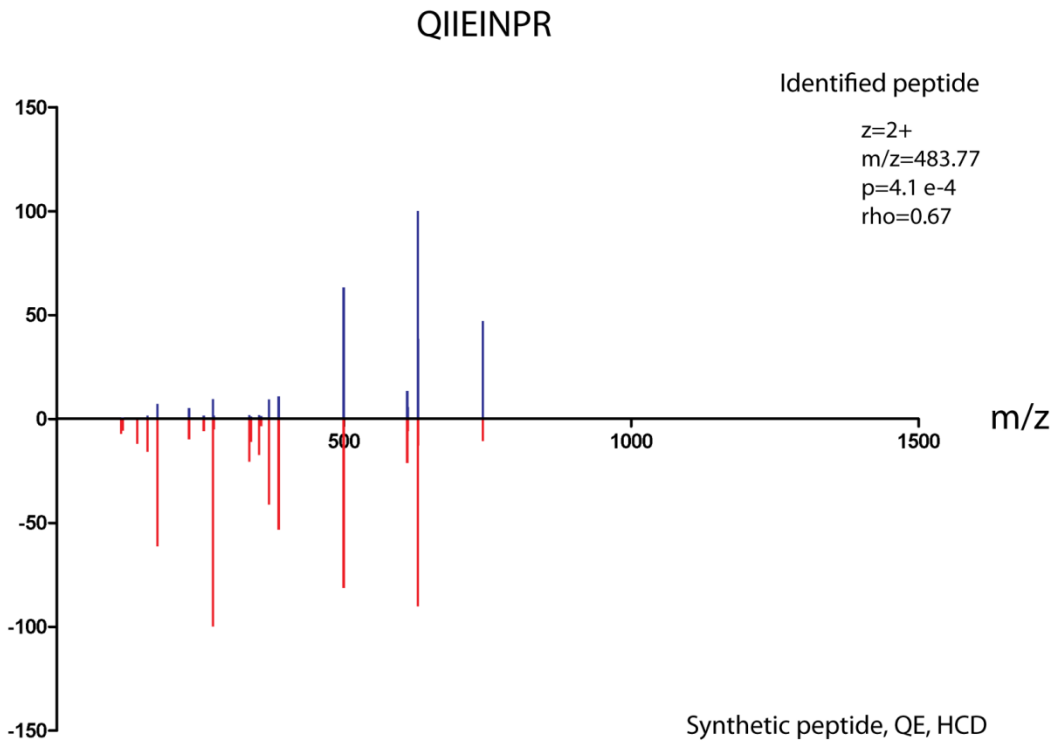


Overlapped Fragmentation Table

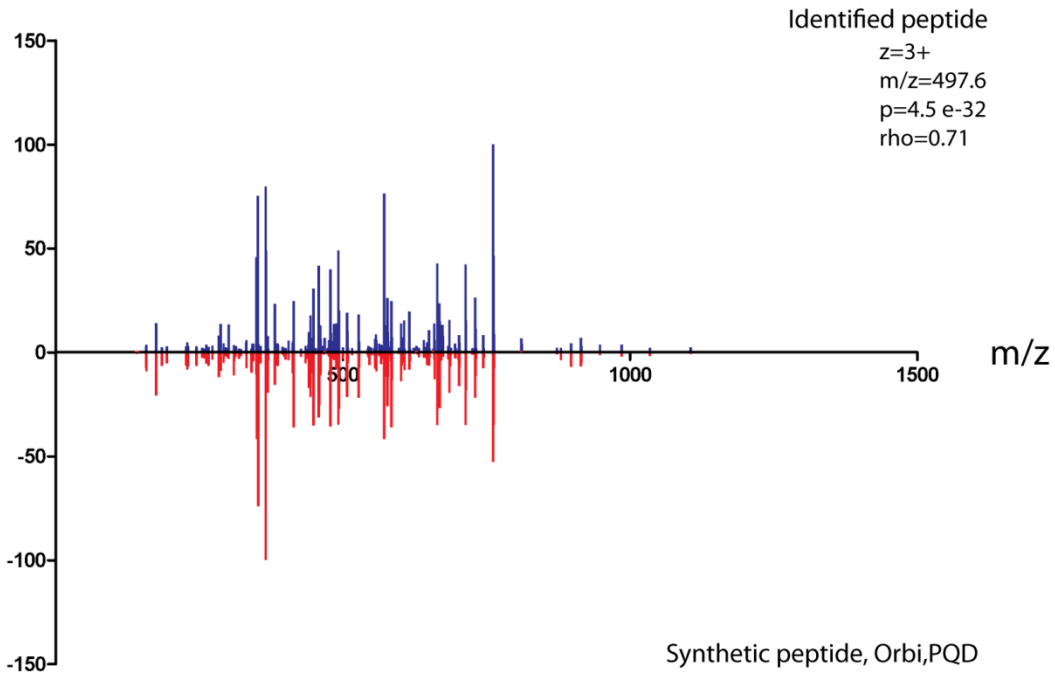
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	344.21	172.61	**N+229**	2,180.34	1,090.67	**15**
2	415.25	208.13	**A**	1,837.14	919.07	**14**
3	528.33	264.67	**L**	1,766.10	883.55	**13**
4	656.39	328.7	**Q**	1,653.02	827.01	**12**
5	785.44	393.22	**E**	1,524.96	762.98	**11**
6	898.52	449.76	**L**	1,395.91	698.46	**10**
7	1,026.58	513.79	**Q**	1,282.83	641.92	**9**
8	1,154.64	577.82	**Q**	1,154.77	577.89	**8**
9	1,267.72	634.36	**I**	1,026.71	513.86	**7**
10	1,380.80	690.91	**I**	913.63	457.32	**6**
11	1,493.89	747.45	**I**	800.54	400.78	**5**
12	1,594.94	797.97	**T**	687.46	344.23	**4**
13	1,691.99	846.5	**P**	586.41	293.71	**3**
14	1,805.07	903.04	**I**	489.36	245.18	**2**
15	2,180.34	1,090.67	**K+229**	376.28	188.64	**1**



Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	341.2		**Q+212**	1,194.70	597.86	**8**
2	454.29		**I**	854.51	427.76	**7**
3	567.37		**I**	741.43	371.22	**6**
4	696.41		**E**	628.34		**5**
5	809.5		**I**	499.3		**4**
6	923.54	462.27	**N**	386.21		**3**
7	1,020.59	510.8	**P**	272.17		**2**
8	1,194.70	597.86	**R**	175.12		**1**

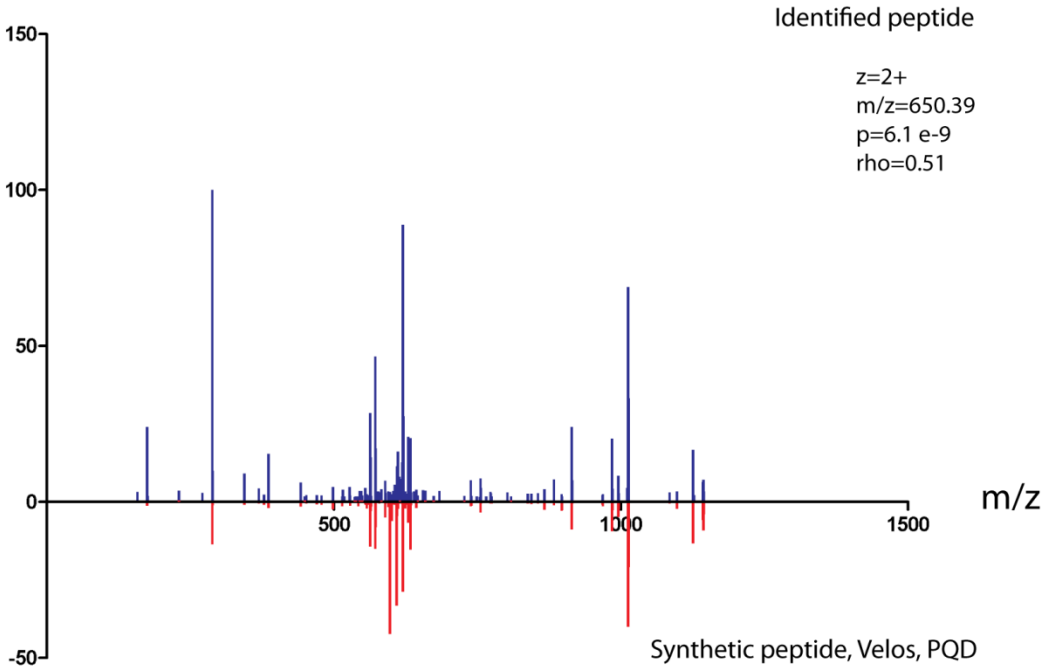
RASGEPSVESSR



Overlapped Fragmentation Table

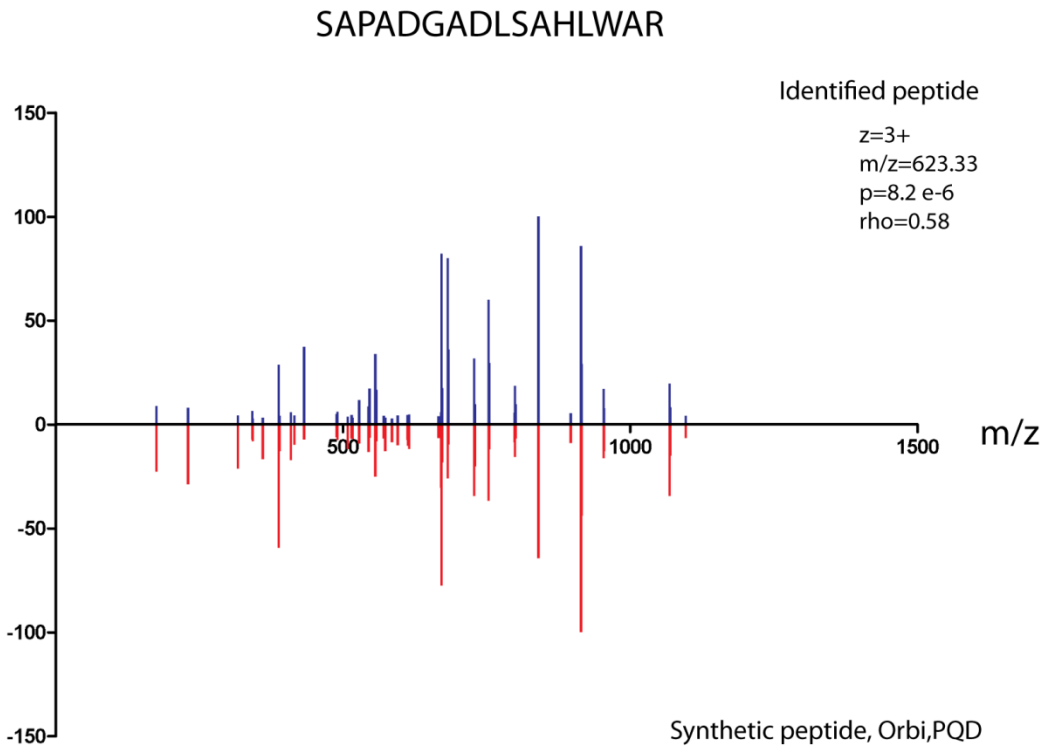
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	386.27	193.64	R+229	1,490.78	745.89	12
2	457.31	229.16	A	1,105.51	553.26	11
3	544.34	272.67	S	1,034.47	517.74	10
4	601.36	301.18	G	947.44	474.23	9
5	730.4	365.71	E	890.42	445.71	8
6	827.46	414.23	P	761.38	381.19	7
7	914.49	457.75	S	664.33	332.67	6
8	1,013.56	507.28	V	577.29	289.15	5
9	1,142.60	571.8	E	478.23	239.62	4
10	1,229.63	615.32	S	349.18	175.1	3
11	1,316.66	658.84	S	262.15	131.58	2
12	1,490.78	745.89	R	175.12	88.06	1

RQQLQELR



Overlapped Fragmentation Table

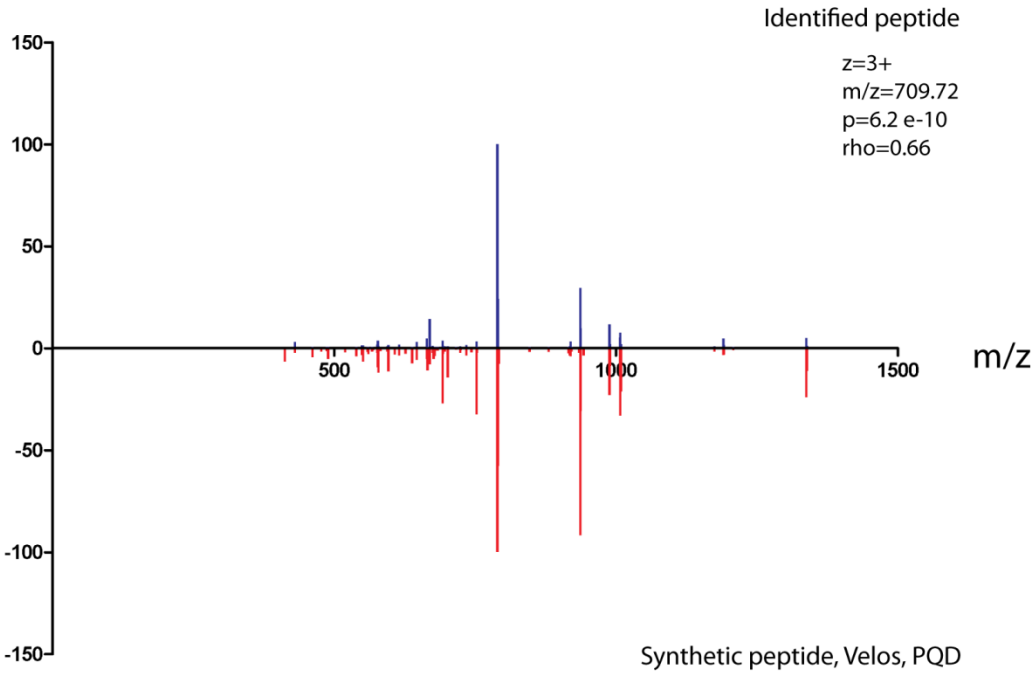
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	386.27	193.64	**R+229**	1,299.77	650.39	**8**
2	514.33	257.67	**Q**	914.51	457.76	**7**
3	642.39	321.7	**Q**	786.45	393.73	**6**
4	755.47	378.24	**L**	658.39		**5**
5	883.53	442.27	**Q**	545.3		**4**
6	1,012.57	506.79	**E**	417.25		**3**
7	1,125.66	563.33	**L**	288.2		**2**
8	1,299.77	650.39	**R**	175.12		**1**



Overlapped Fragmentation Table

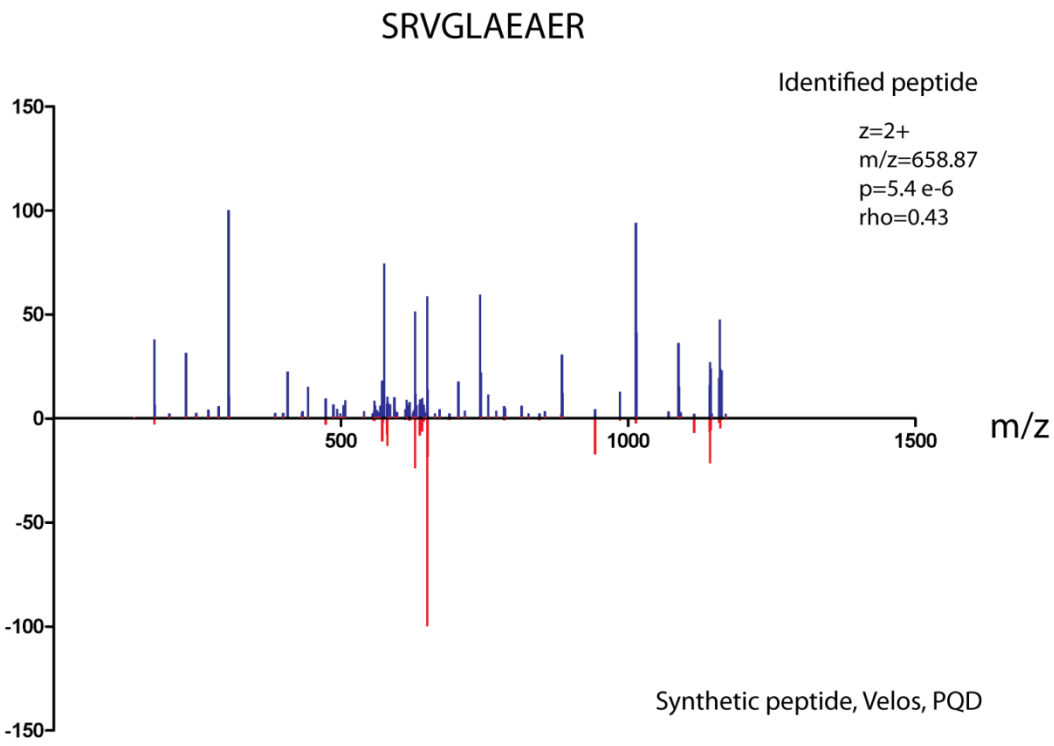
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	317.2	159.1	S+229	1,866.97	933.99	16
2	388.24	194.62	A	1,550.77	775.89	15
3	485.29	243.15	P	1,479.73	740.37	14
4	556.33	278.67	A	1,382.68	691.84	13
5	671.36	336.18	D	1,311.64	656.33	12
6	728.38	364.69	G	1,196.62	598.81	11
7	799.41	400.21	A	1,139.60	570.3	10
8	914.44	457.72	D	1,068.56	534.78	9
9	1,027.53	514.27	L	953.53	477.27	8
10	1,114.56	557.78	S	840.45	420.73	7
11	1,185.59	593.3	A	753.42	377.21	6
12	1,322.65	661.83	H	682.38	341.69	5
13	1,435.74	718.37	L	545.32	273.16	4
14	1,621.82	811.41	W	432.24	216.62	3
15	1,692.85	846.93	A	246.16	123.58	2
16	1,866.97	933.99	R	175.12	88.06	1

SLFSSPASLAFPYSPVAR



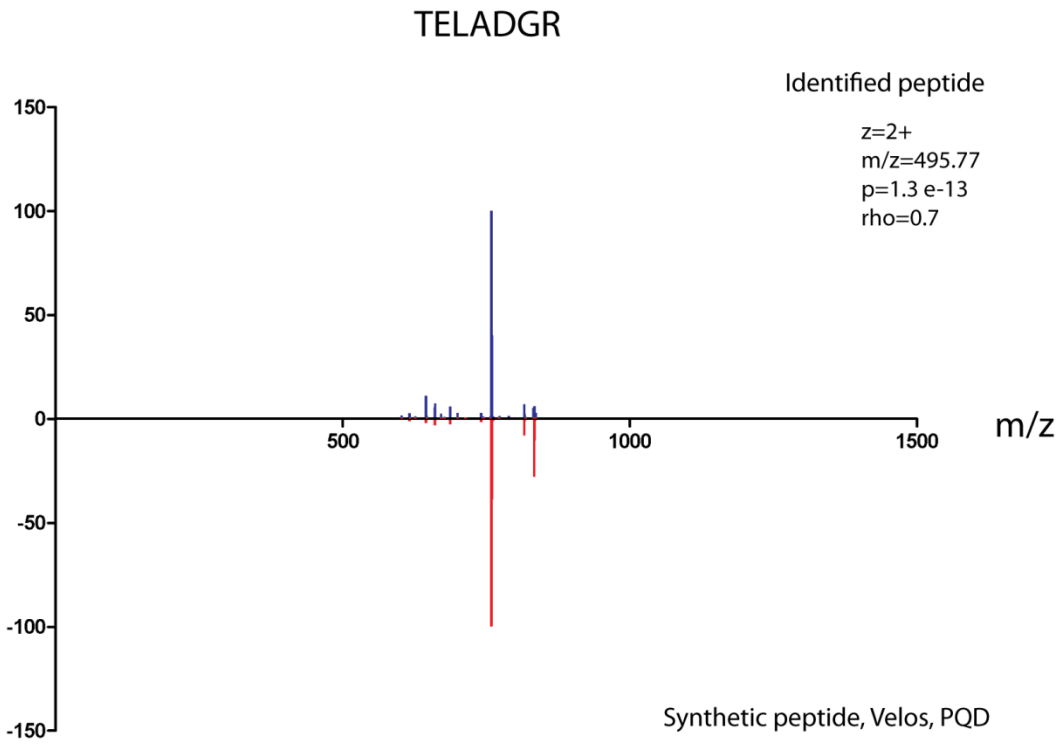
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	317.2	159.1	S+229	2,126.15	1,063.58	18
2	430.29	215.65	L	1,809.95	905.48	17
3	577.35	289.18	F	1,696.87	848.94	16
4	664.39	332.7	S	1,549.80	775.4	15
5	751.42	376.21	S	1,462.77	731.89	14
6	848.47	424.74	P	1,375.74	688.37	13
7	919.51	460.26	A	1,278.68	639.85	12
8	1,006.54	503.77	S	1,207.65	604.33	11
9	1,119.62	560.32	L	1,120.61	560.81	10
10	1,190.66	595.83	A	1,007.53	504.27	9
11	1,337.73	669.37	F	936.49	468.75	8
12	1,434.78	717.9	P	789.43	395.22	7
13	1,597.85	799.43	Y	692.37	346.69	6
14	1,684.88	842.94	S	529.31	265.16	5
15	1,781.93	891.47	P	442.28	221.64	4
16	1,881.00	941	V	345.22	173.12	3
17	1,952.04	976.52	A	246.16	123.58	2
18	2,126.15	1,063.58	R	175.12	88.06	1



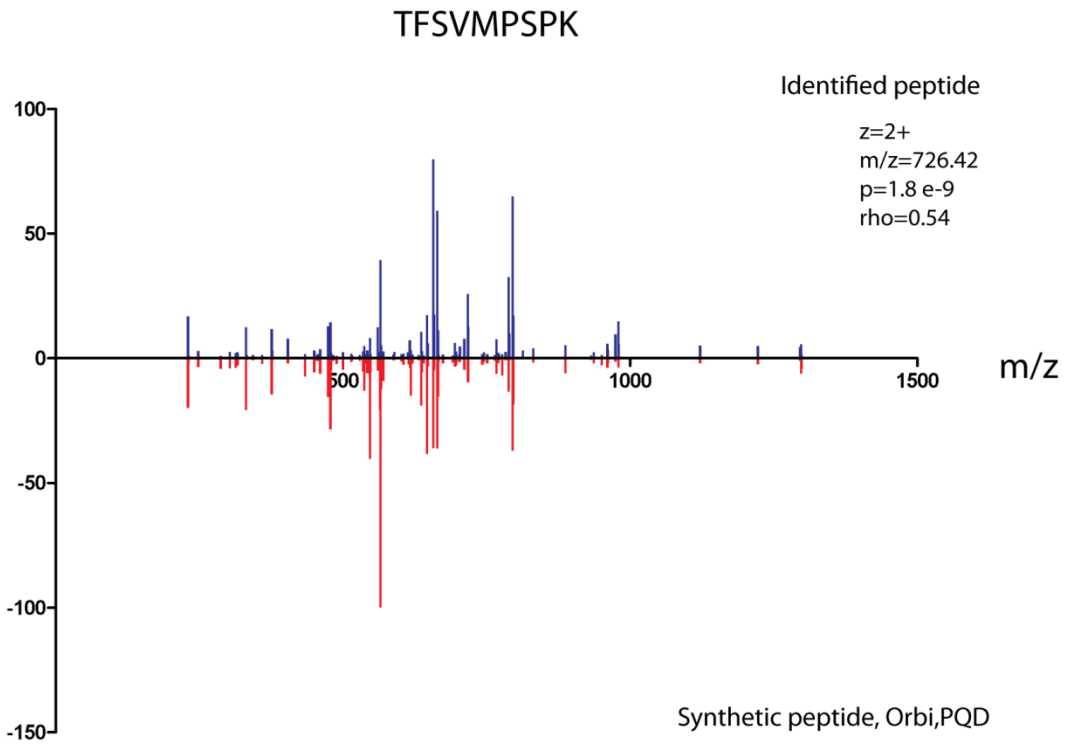
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	317.2		**S+229**	1,316.75	658.88	**10**
2	473.3	237.16	**R**	1,000.55	500.78	**9**
3	572.37	286.69	**V**	844.45	422.73	**8**
4	629.39	315.2	**G**	745.38	373.2	**7**
5	742.48	371.74	**L**	688.36	344.68	**6**
6	813.51	407.26	**A**	575.28		**5**
7	942.56	471.78	**E**	504.24		**4**
8	1,013.59	507.3	**A**	375.2		**3**
9	1,142.64	571.82	**E**	304.16		**2**
10	1,316.75	658.88	**R**	175.12		**1**



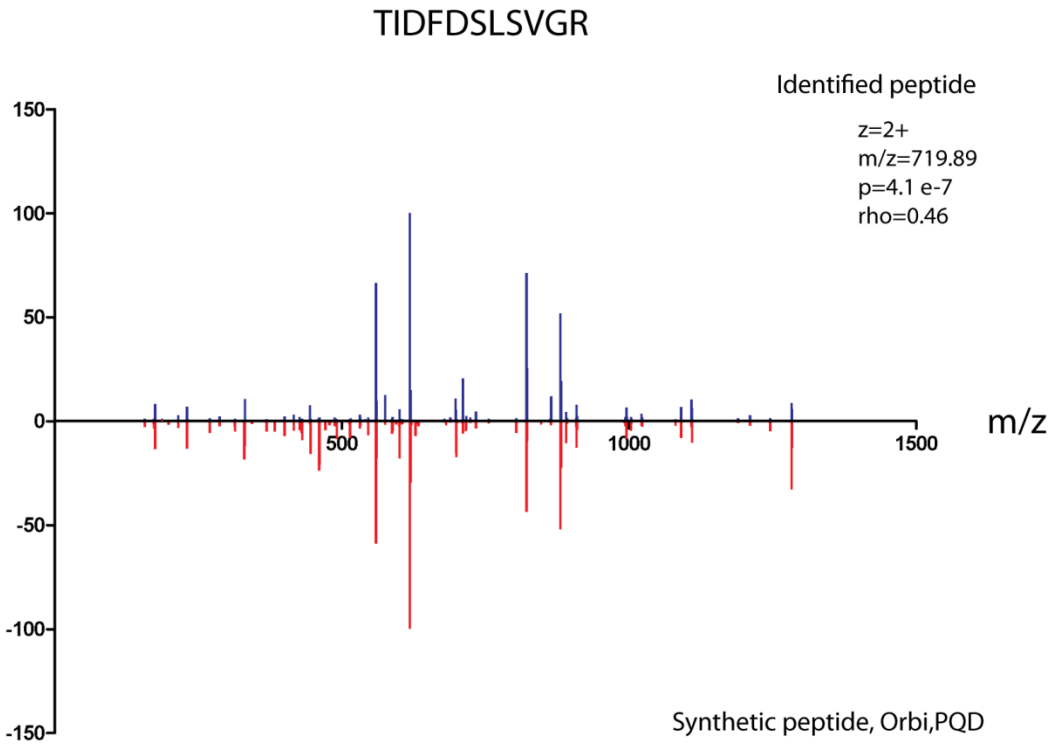
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	331.22		T+229	990.54	495.77	7
2	460.26		E	660.33	330.67	6
3	573.34		L	531.29		5
4	644.38		A	418.2		4
5	759.41		D	347.17		3
6	816.43	408.72	G	232.14		2
7	990.54	495.77	R	175.12		1



Overlapped Fragmentation Table

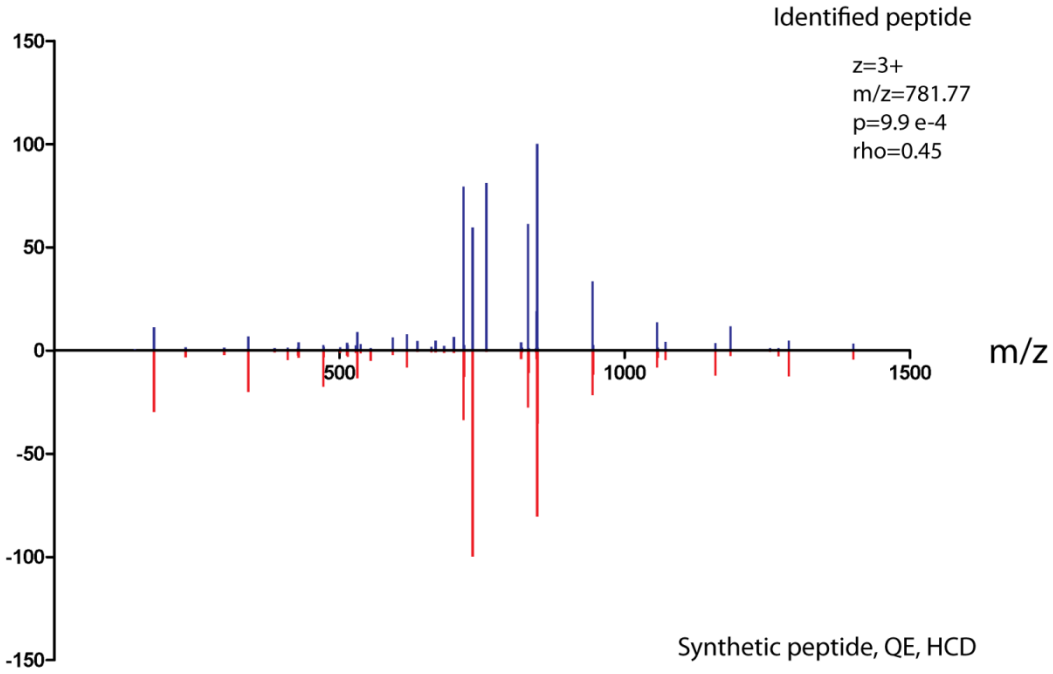
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	331.22		T+229	1,451.83	726.42	9
2	478.29		F	1,121.62	561.32	8
3	565.32		S	974.55	487.78	7
4	664.39		V	887.52	444.26	6
5	795.43		M	788.45		5
6	892.48	446.74	P	657.41		4
7	979.51	490.26	S	560.36		3
8	1,076.56	538.79	P	473.33		2
9	1,451.83	726.42	K+229	376.28		1



Overlapped Fragmentation Table

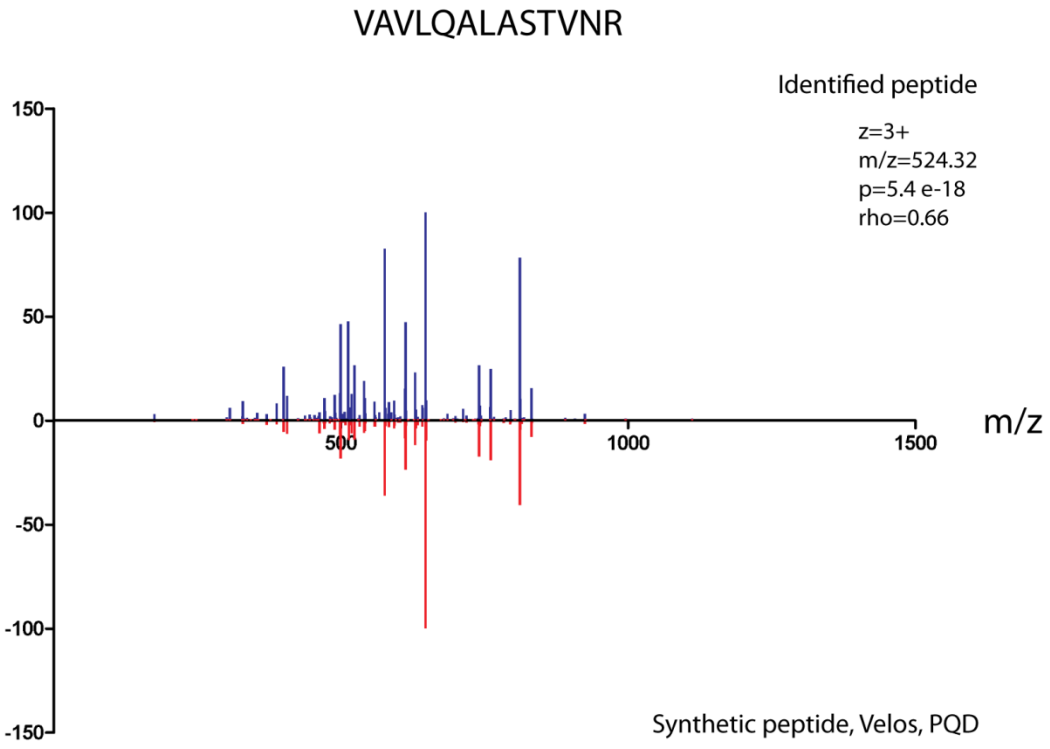
B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	331.22		T+229	1,438.77	719.89	11
2	444.3		I	1,108.56	554.79	10
3	559.33		D	995.48	498.24	9
4	706.4		F	880.45	440.73	8
5	821.42		D	733.38	367.2	7
6	908.46	454.73	S	618.36	309.68	6
7	1,021.54	511.27	L	531.32		5
8	1,108.57	554.79	S	418.24		4
9	1,207.64	604.32	V	331.21		3
10	1,264.66	632.83	G	232.14		2
11	1,438.77	719.89	R	175.12		1

TSTVDLPIESQLLWQLDR



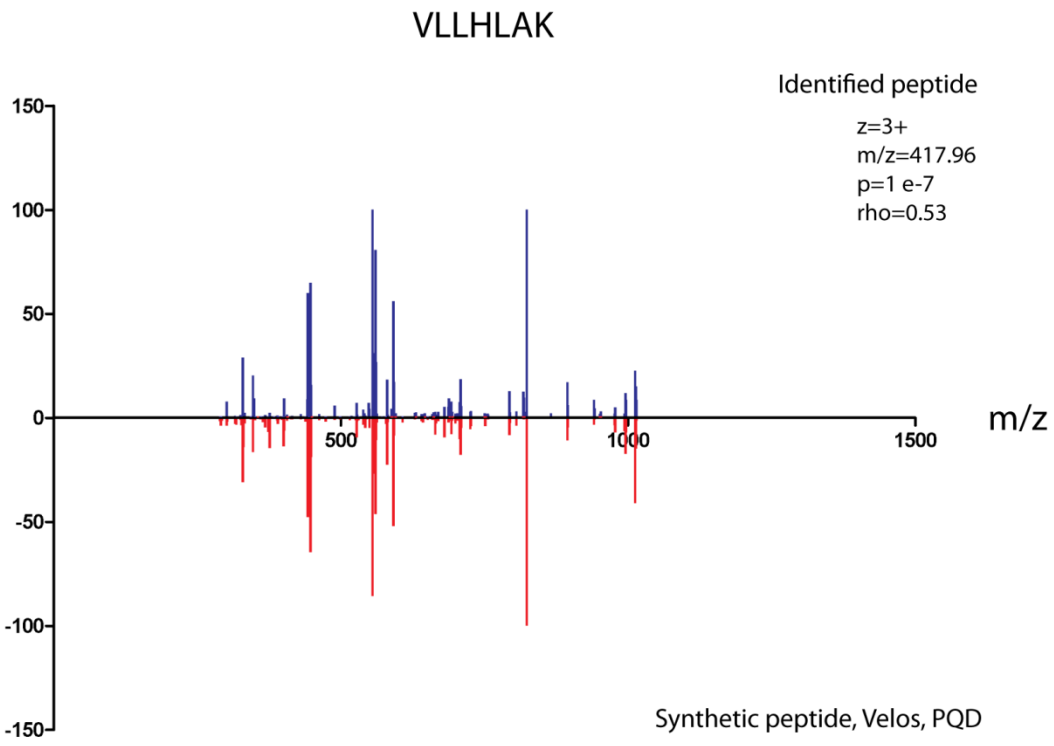
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	331.22	166.11	T+229	2,343.28	1,172.14	18
2	418.25	209.63	S	2,013.07	1,007.04	17
3	519.3	260.15	T	1,926.03	963.52	16
4	618.37	309.69	V	1,824.99	913	15
5	733.39	367.2	D	1,725.92	863.46	14
6	846.48	423.74	L	1,610.89	805.95	13
7	943.53	472.27	P	1,497.81	749.41	12
8	1,056.61	528.81	I	1,400.75	700.88	11
9	1,185.66	593.33	E	1,287.67	644.34	10
10	1,272.69	636.85	S	1,158.63	579.82	9
11	1,400.75	700.88	Q	1,071.59	536.3	8
12	1,513.83	757.42	L	943.54	472.27	7
13	1,626.92	813.96	L	830.45	415.73	6
14	1,812.99	907	W	717.37	359.19	5
15	1,941.05	971.03	Q	531.29	266.15	4
16	2,054.14	1,027.57	L	403.23	202.12	3
17	2,169.16	1,085.09	D	290.15	145.58	2
18	2,343.28	1,172.14	R	175.12	88.06	1



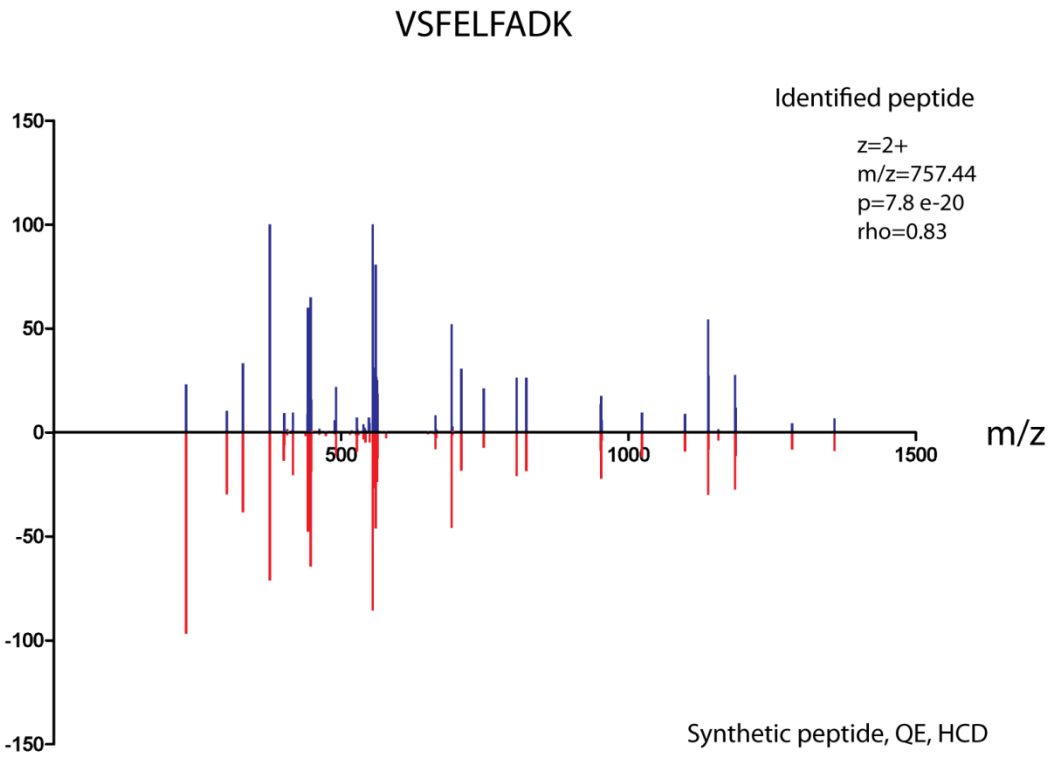
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	329.24	165.12	**V+229**	1,570.95	785.98	**13**
2	400.28	200.64	**A**	1,242.72	621.86	**12**
3	499.34	250.18	**V**	1,171.68	586.34	**11**
4	612.43	306.72	**L**	1,072.61	536.81	**10**
5	740.49	370.75	**Q**	959.53	480.27	**9**
6	811.52	406.27	**A**	831.47	416.24	**8**
7	924.61	462.81	**L**	760.43	380.72	**7**
8	995.65	498.33	**A**	647.35	324.18	**6**
9	1,082.68	541.84	**S**	576.31	288.66	**5**
10	1,183.72	592.37	**T**	489.28	245.14	**4**
11	1,282.79	641.9	**V**	388.23	194.62	**3**
12	1,396.84	698.92	**N**	289.16	145.08	**2**
13	1,570.95	785.98	**R**	175.12	88.06	**1**



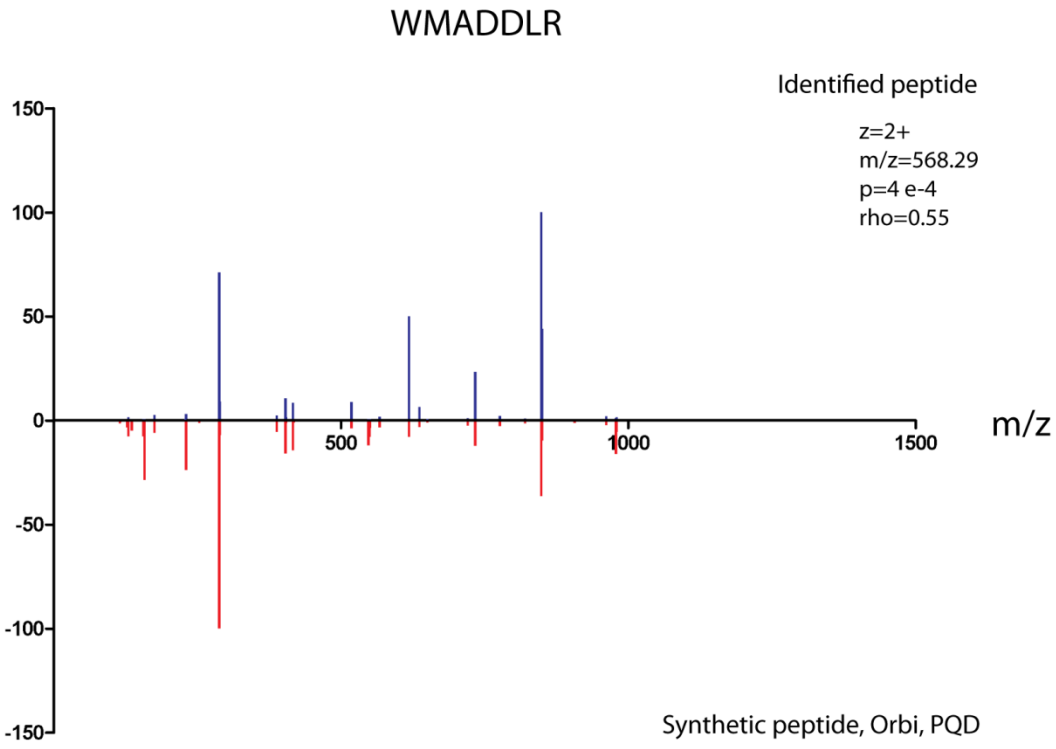
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	329.24	165.12	**V+229**	1,251.86	626.43	**7**
2	442.32	221.66	**L**	923.62	462.32	**6**
3	555.41	278.21	**L**	810.54	405.77	**5**
4	692.47	346.74	**H**	697.46	349.23	**4**
5	805.55	403.28	**L**	560.4	280.7	**3**
6	876.59	438.8	**A**	447.31	224.16	**2**
7	1,251.86	626.43	**K+229**	376.28	188.64	**1**



Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	329.24		**V+229**	1,513.87	757.44	**9**
2	416.27		**S**	1,185.64	593.32	**8**
3	563.34		**F**	1,098.60	549.81	**7**
4	692.38		**E**	951.54	476.27	**6**
5	805.47		**L**	822.49		**5**
6	952.53	476.77	**F**	709.41		**4**
7	1,023.57	512.29	**A**	562.34		**3**
8	1,138.60	569.8	**D**	491.3		**2**
9	1,513.87	757.44	**K+229**	376.28		**1**

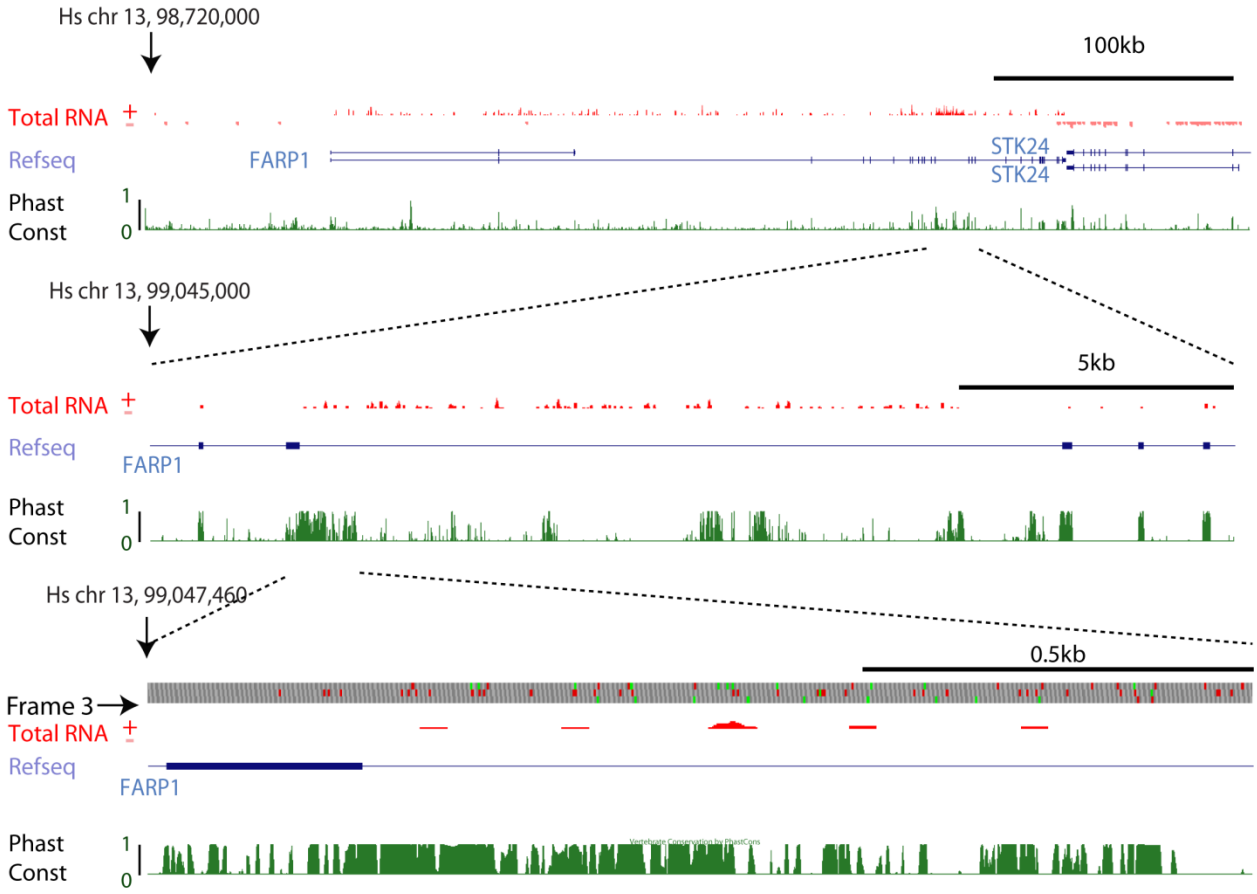


Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	416.25		W+229	1,135.58	568.30	7
2	547.29		M	720.33	360.7	6
3	618.33		A	589.29		5
4	733.35		D	518.26		4
5	848.38		D	403.23		3
6	961.47	481.24	L	288.2		2
7	1,135.58	568.29	R	175.12		1

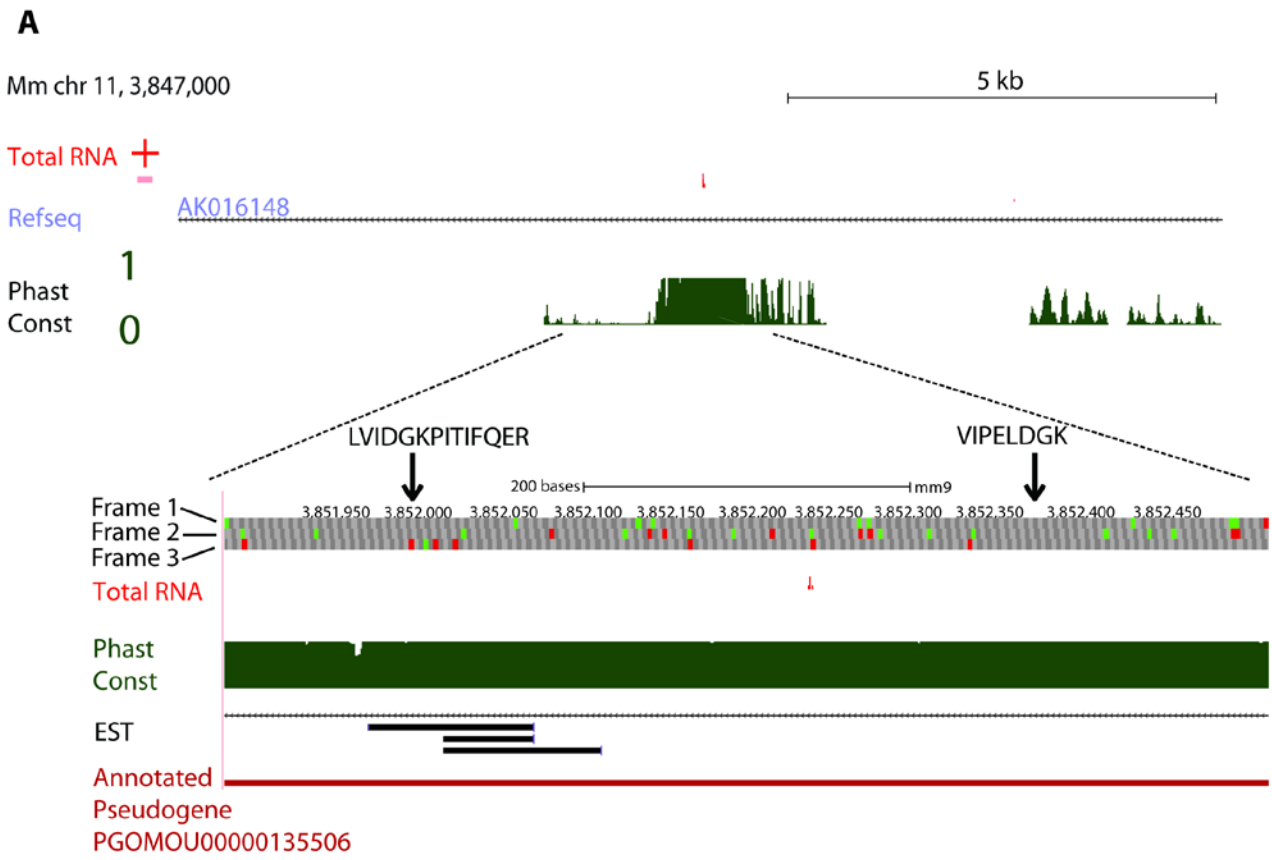
Supplementary Figure 3. Validation of identified spectral matches using synthetic peptides. Spectra of 41 identified novel peptides (top) were compared and statistically validated to synthetic peptides (bottom). All these peptides show a strong positive rank-ordered Spearman correlation coefficient with a significant p-value of less than 0.05. The fragmentation table indicates the y and b ion series for the peptides, ions depicted in green color indicate that they were identified in both the spectra, ions depicted in blue color were identified only in 'identified peptide spectra' and ions depicted in pink color were identified only in synthetic peptide spectra (see Methods). Including Figure 2E, Supplementary Figure 2B, Supplementary Figure 3, Supplementary Figure 5B and Supplementary Figure 7C, a total of 45 novel peptides were validated.

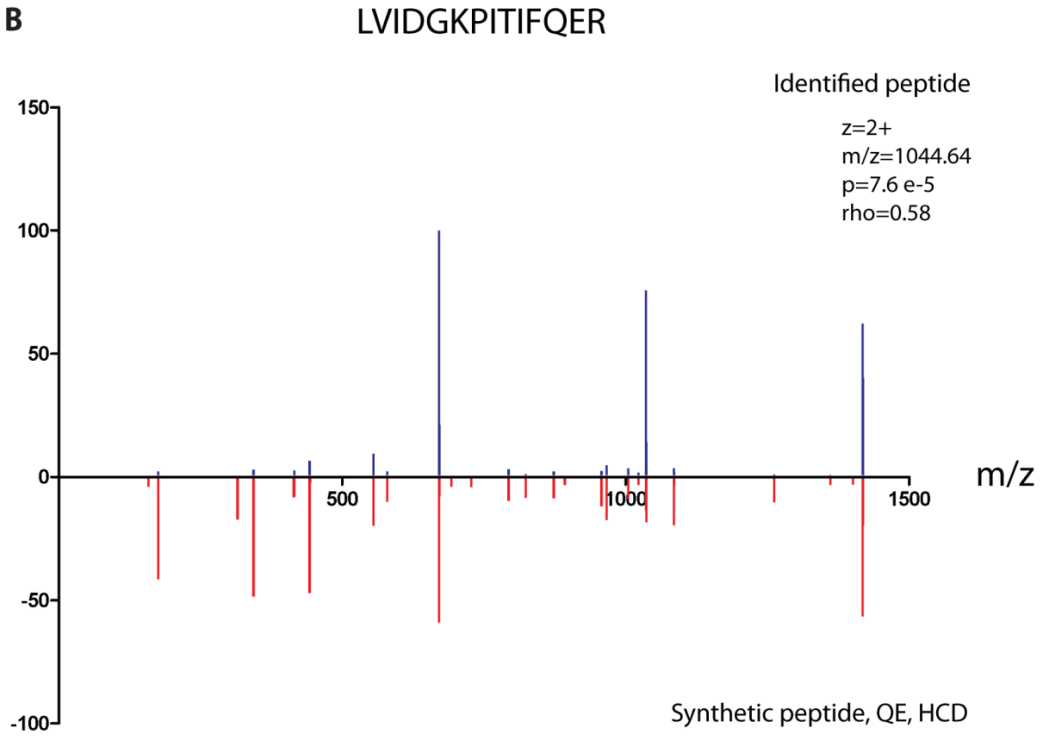
Supplementary Figure 4 **Steen**



Supplementary Figure 4. A screenshot from the UCSC genome browser of the FARP1 locus from human with RNA-seq data from HeLa cells. Intron 13 (magnified) is similar to mouse with an elevated level of expression (Figure 2A). The top track in the bottom panel indicates stop codons (red) and start codons (green). The third frame has an amino acid sequence which is consistent with the longer exon.

Supplementary Figure 5 **Steen**

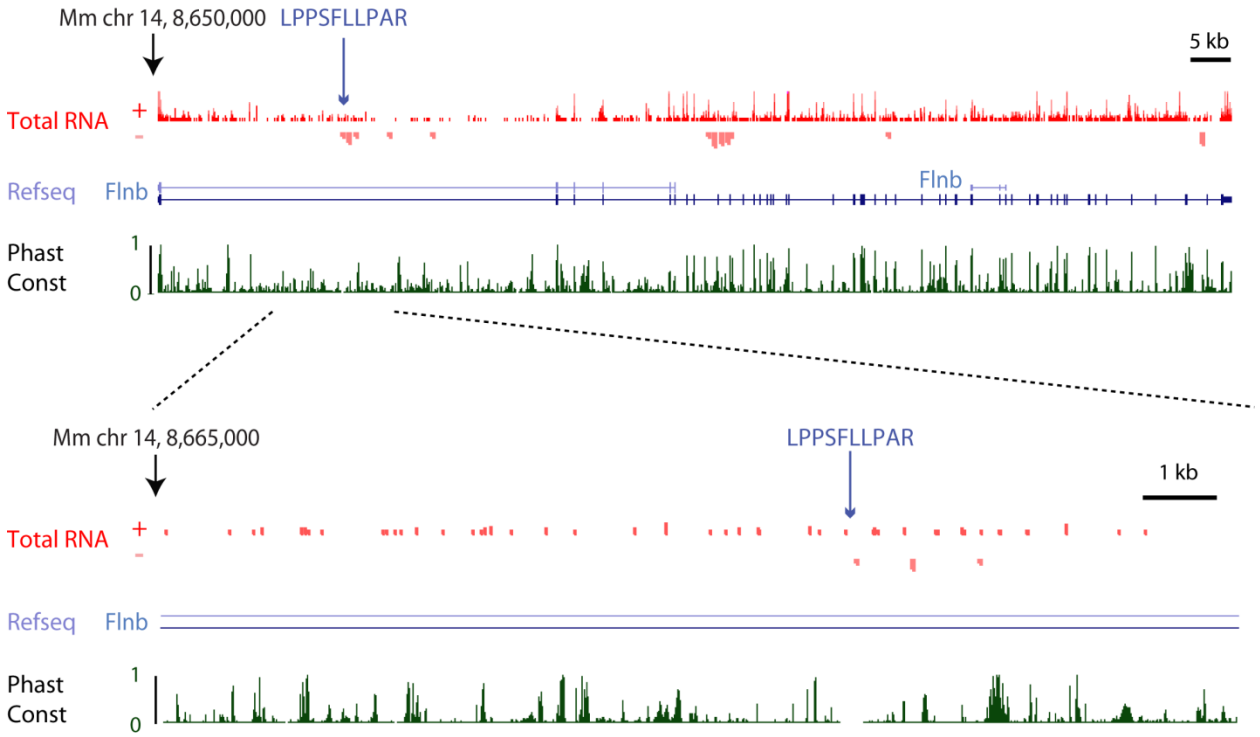




Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25		L+229	2,087.26	1,044.14	14
2	442.32		V	1,745.02	873.01	13
3	555.41		I	1,645.95	823.48	12
4	670.43		D	1,532.86	766.94	11
5	727.46		G	1,417.84	709.42	10
6	1,084.71	542.86	K+229	1,360.82	680.91	9
7	1,181.77	591.39	P	1,003.56	502.28	8
8	1,294.85	647.93	I	906.5	453.76	7
9	1,395.90	698.45	T	793.42	397.21	6
10	1,508.98	754.99	I	692.37		5
11	1,656.05	828.53	F	579.29		4
12	1,784.11	892.56	Q	432.22		3
13	1,913.15	957.08	E	304.16		2
14	2,087.26	1,044.14	R	175.12		1

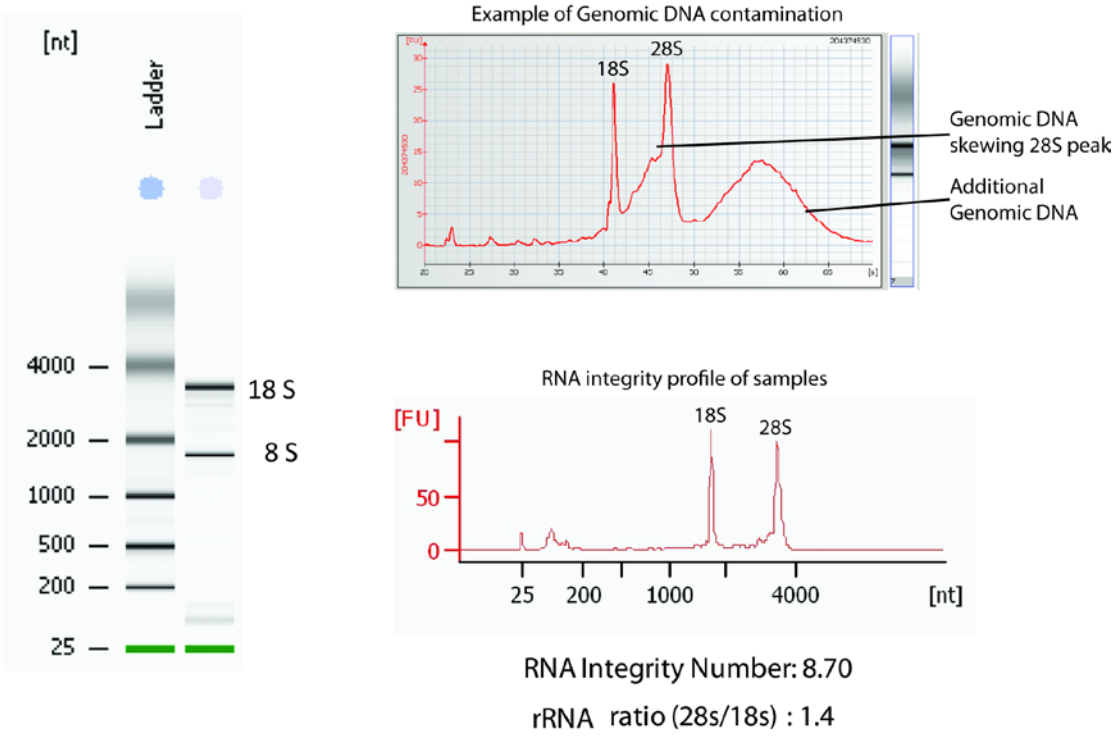
Supplementary Figure 5. Spectral validation data for a pseudogene (A) Screenshot showing two peptides from the pseudogene PGOMOU00000135506 on chromosome 11 (number 13 in Supplementary Figure 7B). The format and conventions are as in Figure 2A. **(B)** Experimental and synthetic spectra validation for the first peptide LVIDGKPITIFQER.



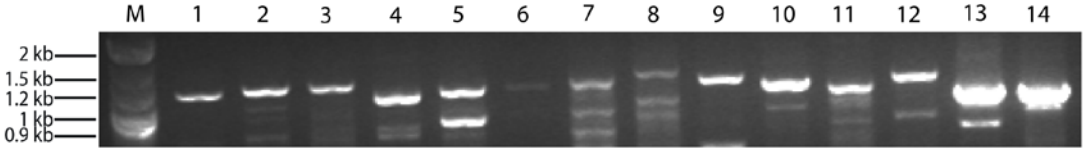
Supplementry Figure 6. Screenshot from the UCSC genome browser of the Flnb locus from mouse.

Supplementary Figure 7 **Steen**

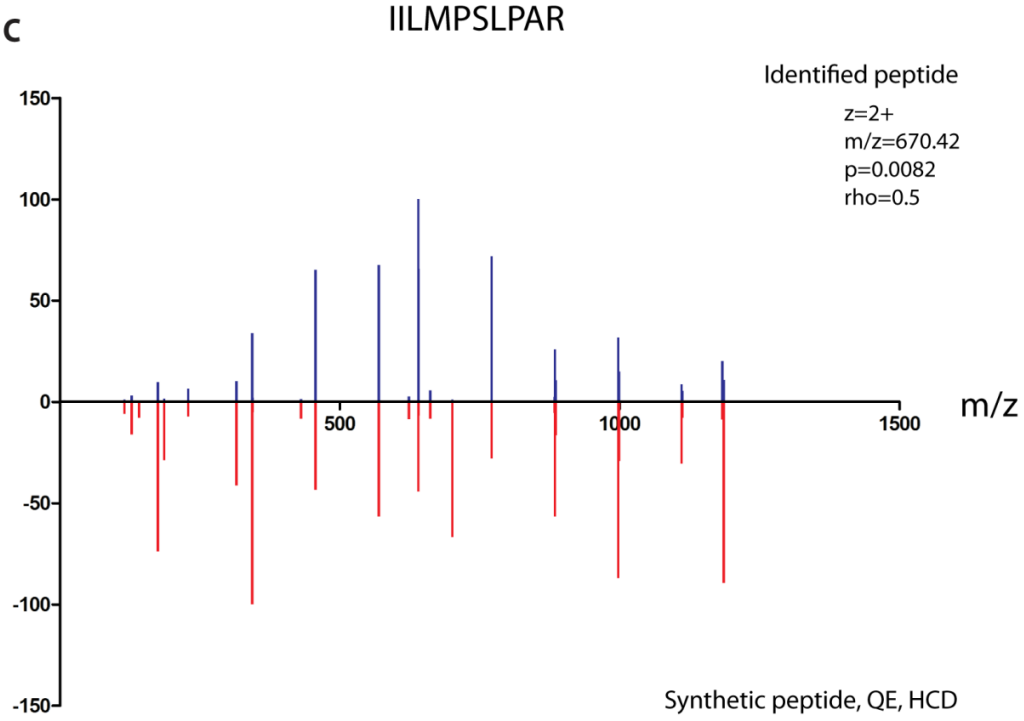
A



B



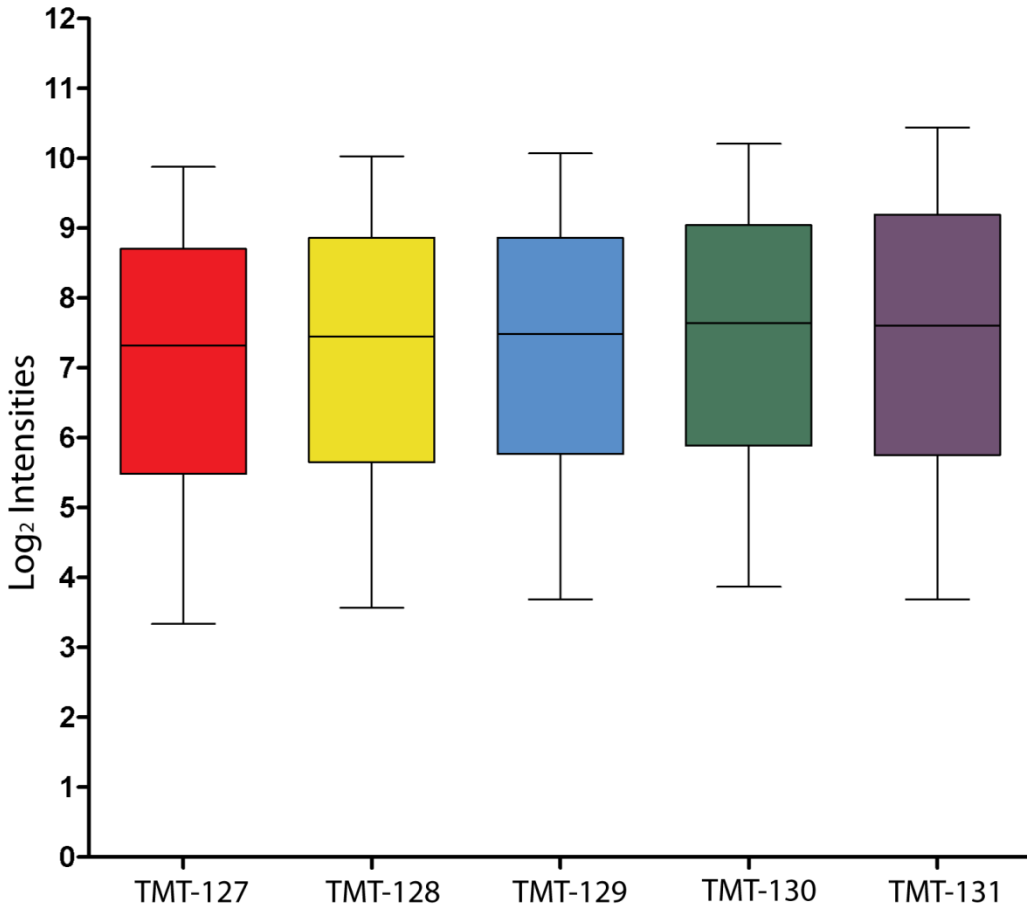
1 Suvn (g1) - 1325 bp
2 Armc9 (g3) - 1396 bp
3 Grpbp10 (g4) - 1473 bp
4 Elmo2 (g4) - 1177 bp
5 E13006D01Rik (g5) - 1310 bp
6 Cacna23d (g4) - 1278 bp
7 Gprk5 (g4) - 1394 bp
8 Nars2 (g4) - 1549 bp
9 Cox17 (g4) - 1367 bp
10 Mlstd2 (g4) - 1243 bp
11 Fars2 (g4) - 1155 bp
12 St6galnac3 (g4) - 1295 bp
13 PGOMOU00000135506 (g2) - 1002 bp
14 PGOMOU00000135766 (g2) - 1008 bp



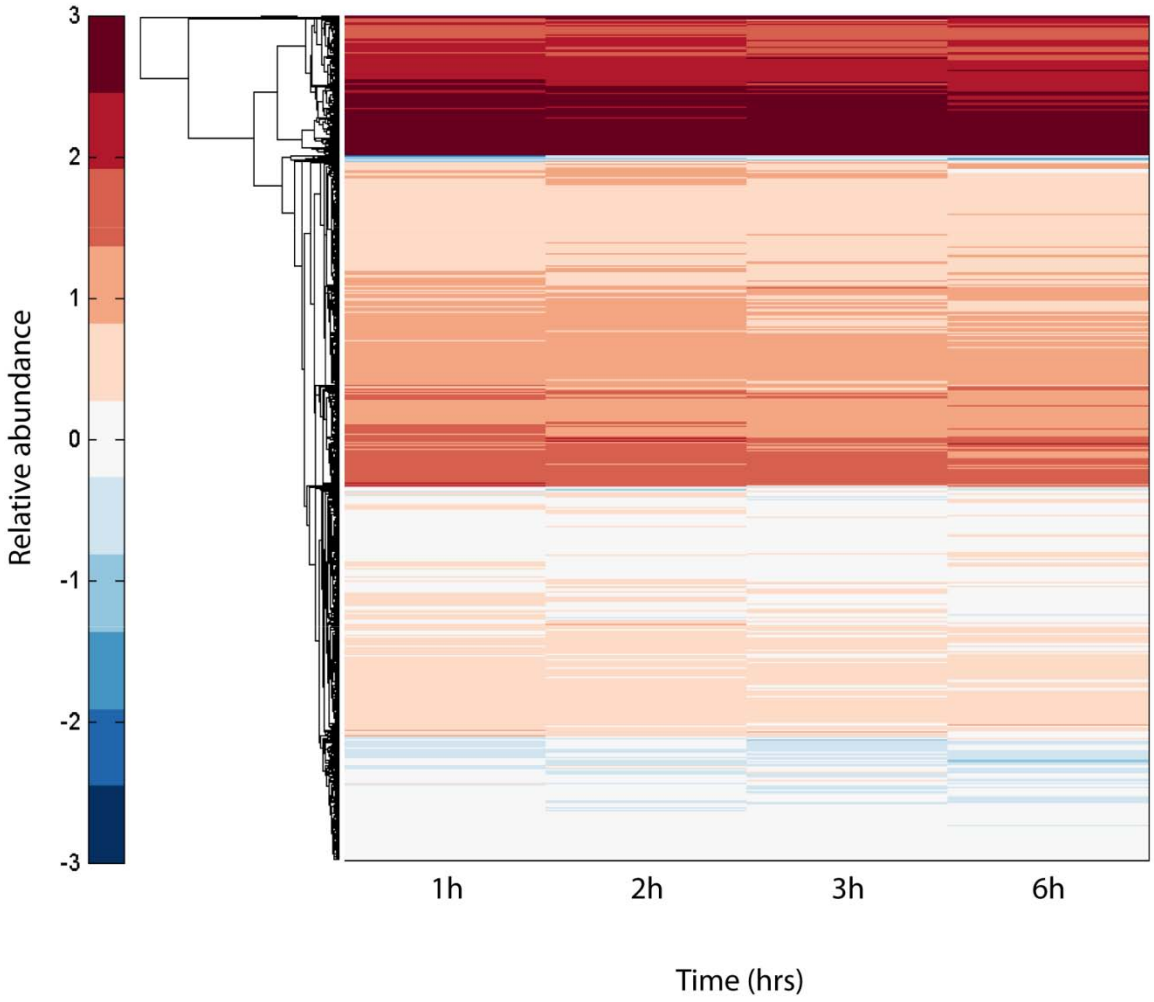
Overlapped Fragmentation Table

B	B Ions	B+2H	AA	Y Ions	Y+2H	Y
1	343.25		I+229	1,339.83	670.42	10
2	456.34		I	997.59	499.3	9
3	569.42		L	884.5	442.75	8
4	700.46		M	771.42	386.21	7
5	797.52		P	640.38	320.69	6
6	884.55	442.78	S	543.32		5
7	997.63	499.32	L	456.29		4
8	1,094.68	547.85	P	343.21		3
9	1,165.72	583.36	A	246.16		2
10	1,339.83	670.42	R	175.12		1

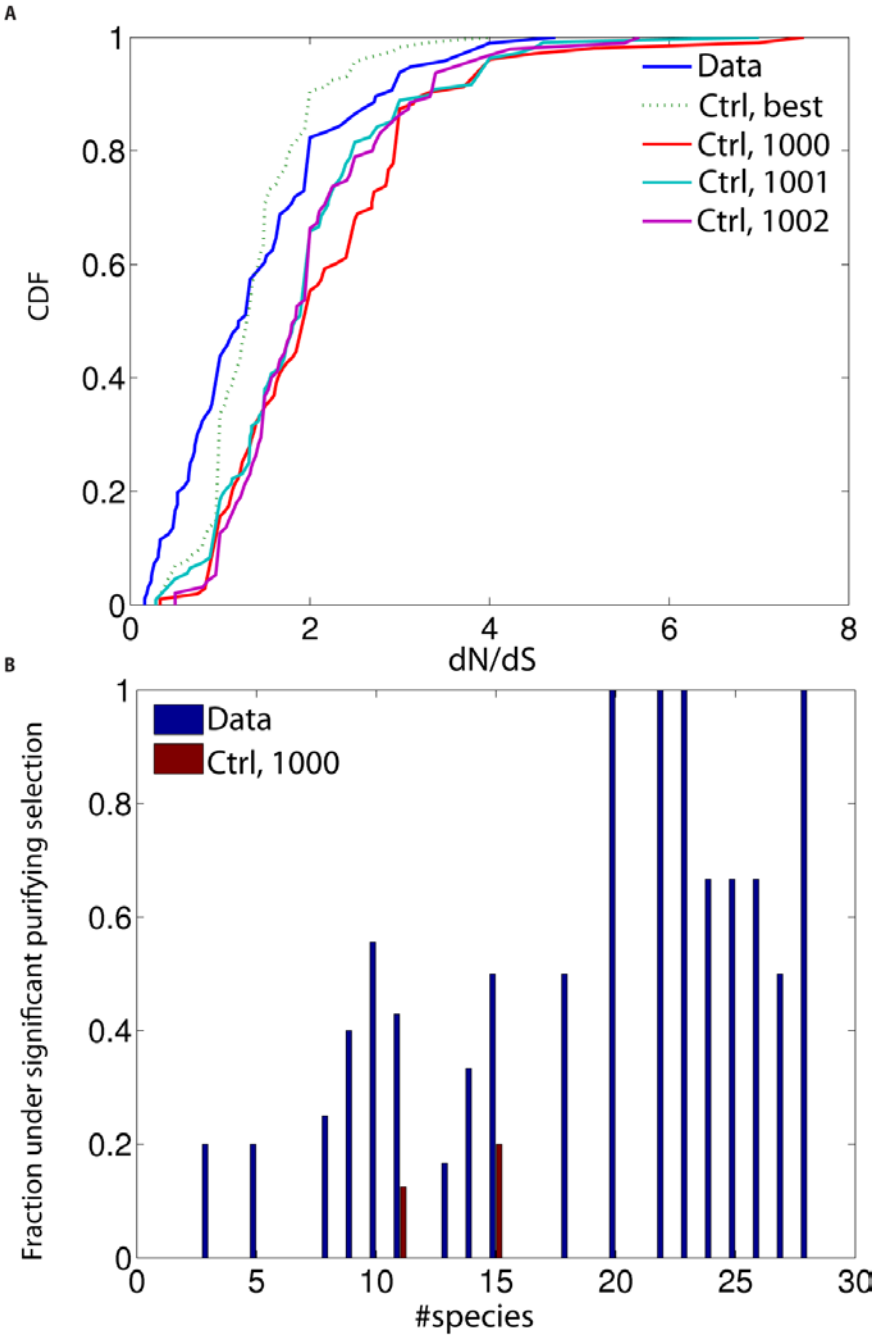
Supplementary Figure 7. Validation of novel peptides in extragenic regions. (A) RNA integrity profile from bioanalyzer showing DNA-free, high quality and intact RNA. The shaded spectrum is hypothetical example for presence of genomic DNA shown as reference from bio analyzer. **(B)** RT-PCR for 14 different anti-sense loci (C) Validation of Identified and synthetic peptide spectra for the novel peptide overlapping the anti-sense region of Cox17 (IILMPSLPAR). The format and conventions are the same as in Figure 2E. The anti-sense peptide to Cox17 is located at position 38,351,276 on chromosome 16, overlapping but anti-sense to the second intron.



Supplementary Figure 8. Comparison of median intensities across TMT channels for peptides in the dataset. The box plots from median intensities values of log_2 intensities of all peptides among different TMT channels are represented. The data show that there is no quantitative bias in the labeling for each channel.

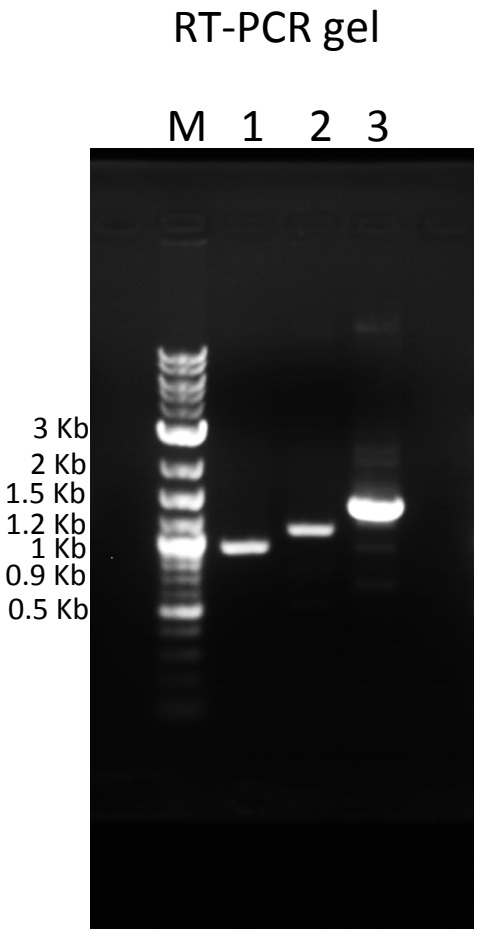


Supplementary Figure 9. Quantitative regulation of known proteins. Hierarchical clustering of the intensity temporal profiles for known proteins (3284). Each row represents one protein. The four columns indicate abundance at 1h, 2h, 3h and 6h post KCl stimulation. The colors represent up- or down-regulation with respect to the 0h time-point (see color map on left, arbitrary units). The clustering reveals several distinct regulatory patterns present both for known.

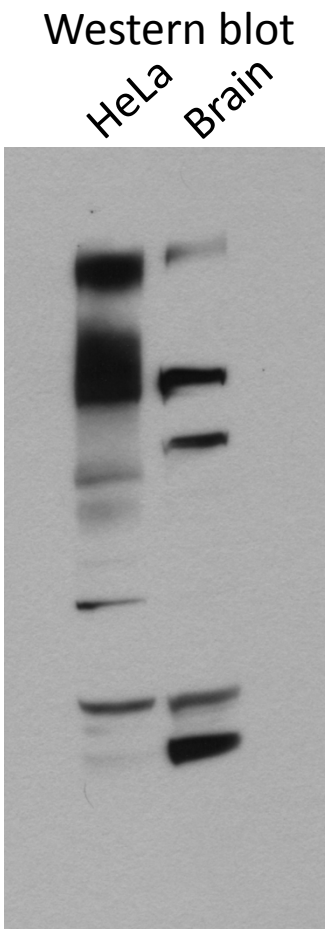


Supplementary Figure 10. Phylogenetic comparisons of novel peptides (A) Distribution of dN/dS ratios for peptides and controls. The controls were chosen either 1000, 1001 or 1002 bps downstream of the novel peptides. As a more strict control (Methods) the dN/dS ratio for the best of the three control frames for each peptide was used (dotted line). The dN/dS ratio is lower for the data compared to both the stringent control (p-value<0.01, KS-test) and the less stringent (p-value<0.0001, KS-test). **(B)** Fraction of peptides with dN/dS ratio<0.8 as a function of the number of species where the sequence was successfully mapped.

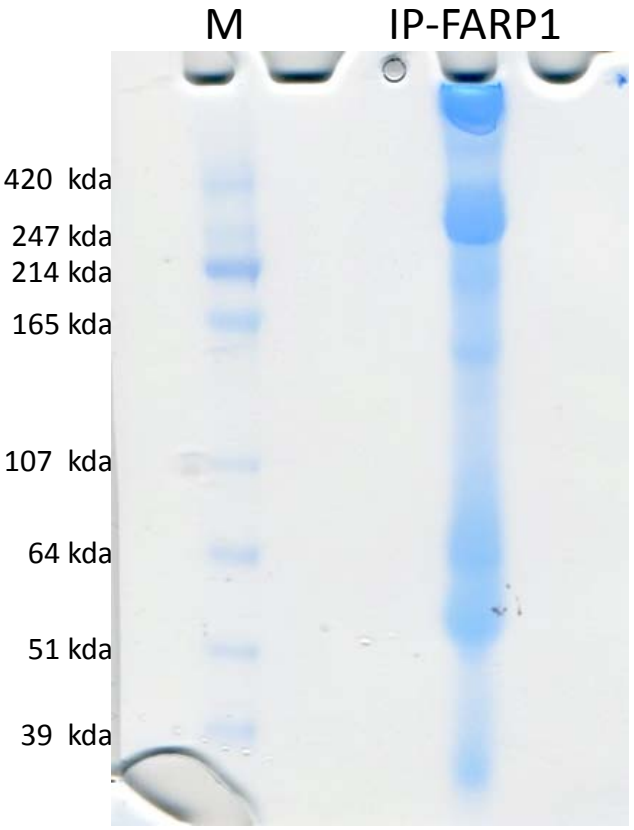
Full gel image of Figure 2C



Full gel image of Figure 2D



Full gel image of Figure 2D



Supplementary Figure 11. Full gel images of Figure 2C and Figure 2D

Supplementary Table 1

#peptide	no_copies	chr	pos	strand	RNA_1h	RNA_6h	1h	2h	3h	6h	validated_I	BLAST_search	Ribosomal	dNdS	overlapping_gene_r	category
AAAAGPGAASEHR	1	1	91478037	1	-0.613	0.648	1.1	1.69	1.87	1.22	1	-	1	NaN	Centg2	Novel internal exon
AADIQGASLGPRK	1	7	1.48E+08	1	-0.309	1.85	-0.00896	0.475	-0.447	-0.211	0	-	0	1.08	Cox8b	Short alternative ORF
AAEDEEVPAFFK	10	14	67529554	0	-0.249	1.04	-0.14	0.188	0.0406	0.0717	1	-	0	NaN	-	Alternative 5' start
AAPPPICPSTALCPCLAR	1	2	33420519	0	-0.585	-0.644	-2.6	-0.399	-0.608	1.13	0	-	0	NaN	Lmx1b	Overlaps intron
AAVSIAEER	1	1	91567439	1	-0.613	0.648	0.463	0.971	1.16	0.312	0	-	0	0.667	Centg2	AS
ACQSMLNTGIIIFK	1	2	1.65E+08	0	-0.263	-1.42	0.385	0.379	-0.435	-0.122	0	-	0	2.6	Elmo2	Divergent
AGVTPASQNR	1	X	20939669	1	0.17	2.79	-1.09	0.0414	-0.0426	-0.317	0	-	0	NaN	EG331392	Pseudogene (BLAST)
AILQALVK	1	X	84544638	0	-0.371	0.76	0.713	0.292	0.654	0.902	0	-	0	NaN	Il1rapl1	AS
AILQGLLK	1	5	1.37E+08	0	-0.387	-1.21	0.713	0.292	0.654	0.902	0	-	0	NaN	Cutl1	Overlaps intron
AIVLIPK	1	9	60250275	0	0	0	0.0745	0.169	-0.19	0.0861	0	-	0	NaN	Thsd4	Overlaps intron
ALIQAVIK	5	7	1.21E+08	1	0.0998	0.95	0.481	0.196	0.434	0.264	1	-	0	1.11	Mlstd2	AS
ALLQALVK	1	7	1.04E+08	1	0.447	1.92	0.713	0.292	0.654	0.902	0	-	0	NaN	Nars2	AS
ALVLIPK	1	2	32434758	1	-0.21	-1.65	0.0745	0.169	-0.19	0.0861	0	-	0	NaN	Pip5kl1	AS
ANLGGLWLL	1	18	64518528	1	-0.103	0.427	1.27	2.18	-0.459	0	0	-	0	1.83	Onecut2	AS
APEGSREGVR	1	9	1.21E+08	0	-0.737	0.678	0.898	1.1	0.184	-0.0301	0	-	0	NaN	Ulk4	Overlaps intron
APFRLCPLPVEK	1	5	67827299	1	1.58	3.37	0.25	0.335	-0.279	0.0821	0	-	0	2.5	EG666938	Putative ncRNA
ASGAPSGSATAPAER	2	2	25066765	0	-0.397	-1.25	-0.524	-0.261	0.979	1.19	0	-	1	NaN	A730008L03Rik	Alternative 5' start
ASGEPSVESSR	6	14	67529332	0	-0.249	1.04	0.293	0.64	0.312	0.0562	1	-	0	1.33	-	Alternative 5' start
ASSSILINEAEPTTDIQIR	1	5	49944247	0	-0.348	0.363	0.0874	-0.628	0	-0.208	0	ASSSILINEAEPTTNIQIR	0	0.329	EG433885	Pseudogene
ATWAVARR	1	10	70891149	1	0	0	-0.149	-0.32	0.545	0.957	0	-	0	NaN	-	AS
AVCLLSNTTAIAEAWAR	1	12	52234717	0	1.51	-1.57	0.655	-0.333	1.01	-0.298	1	-	0	0.429	-	Pseudogene (BLAST)
AYHEQLSVAEITNVCFEPTNQMVK	1	17	5111198	1	-0.559	0.0766	-0.744	-0.956	-0.317	-1.17	0	AYHEQLSVAEITNVCFEPANQMVK	1	0.239	Arid1b	Pseudogene
CDFPYLVLWVQFR	2	16	42107151	1	0	0	-0.0268	0.599	0.415	0.891	0	-	0	NaN	Lsamp	AS
CLLAAGRGLR	1	16	23133852	1	0.704	3.25	-0.268	1.66	1.42	-0.253	0	-	0	NaN	-	Putative ncRNA
CPFLLMRTLR	1	8	80130867	0	0	0	1.15	0.111	1.06	0.627	0	-	0	4	Tmem34	Overlaps intron
CPGNLFEGGR	2	X	1.03E+08	0	-0.113	-1.73	-0.131	-0.52	-0.21	-0.779	0	-	0	3	-	Short alternative ORF
CPTDCTRTLR	1	14	66988529	0	-0.322	0.263	0	0	0	0	0	-	0	1	-	Overlaps intron
CSSPPHCTR	1	3	32436586	1	-0.417	-0.423	0.153	0.208	0.389	-0.706	0	-	1	NaN	Mfn1	AS
DAVAGIR	1	2	1.68E+08	0	-0.2	-0.645	0	0	0	0	0	-	1	NaN	Dpm1	AS
DDLGLGAR	1	7	91104662	0	-0.7	0	0.851	0.881	0.462	0.389	0	-	0	NaN	9930013L23Rik	Overlaps intron
DDQECLLLCQR	1	1	37813851	0	-0.551	-0.277	0.899	0.971	1.31	-0.0469	0	-	0	1.75	Tsga10	Overlaps intron
DEDGLGLR	1	3	1.53E+08	0	-0.585	0.29	0.567	0.633	-0.312	-0.343	0	-	0	1.33	St6galnac3	Overlaps intron
DEDVAGLR	2	16	3969222	0	0	0	0.277	0.428	0.0619	0.192	0	-	0	NaN	Nlrc3	Alternative 3' end
DELGALDQGR	1	4	1.02E+08	0	0	0	-1.35	-1.04	-0.142	-0.958	0	-	0	2.33	B020004J07Rik	AS
DGIRPSNPQPPQPSTGPASR	1	14	1.22E+08	1	-0.466	0.93	-1.35	-1.49	-0.433	-0.663	0	-	1	NaN	Farp1	Overlaps intron
DKPANVQPYYLYGSK	2	11	46053502	0	-0.662	0.572	0.489	0.577	0.731	1.04	1	-	0	0.267	Cyfip2	UCSC (BLAST)
DLYLPLLLQRNILR	2	4	1.3E+08	1	-0.613	-1.7	0.237	-0.287	0.324	0.913	0	-	0	NaN	Sdc3	eRNA
DMCISSDTLGVSDR	1	3	1.58E+08	0	-0.268	1.75	0.914	0.421	1.32	1.51	0	-	0	NaN	-	Alternative 3' end
DQLVDAR	1	18	80860859	0	0.17	0.907	0.851	0.881	0.462	0.389	0	-	0	NaN	Nfatc1	AS
DVAHLGPDPHR	10	14	67529377	0	-0.249	1.04	0.249	0.514	0.789	0.516	1	-	0	0.783	-	Alternative 5' start
DVQQYILHR	5	3	38356427	0	-0.277	1.11	-0.126	0.991	1.03	0.396	0	-	0	0.235	-	Novel internal exon
EDSLLMQILR	1	14	87169352	0	-0.193	1	0.172	0.0369	0.378	0.901	0	-	0	NaN	Diap3	Overlaps intron
EDYYNPSR	1	4	28748296	1	-0.581	0.0765	-0.101	-0.068	0.791	-1.37	0	-	0	2	Epha7	AS
EEEMRDTNESTNTR	1	13	36082831	0	-0.628	-0.28	-0.302	-0.247	-0.373	-0.863	0	-	0	NaN	LOC100042773	Pseudogene (BLAST)
EIGGGGEIR	1	1	84400192	0	-0.272	-0.175	0.293	0.161	0.285	-0.035	0	-	0	1.58	Dner	AS
EMESRDEEVEEAR	1	11	77659932	1	-0.801	1.33	0.361	-0.153	0.716	0.454	0	-	0	NaN	Myo18a	UCSC (BLAST)
EQDGLFSFCLR	1	6	64474513	1	-0.348	0.837	-2.34	0.271	0.578	0	1	-	0	NaN	Grid2	Overlaps intron
EQSTGGTLLR	1	1	1.62E+08	0	-0.737	0.547	0.697	0.945	0.383	0.4	0	-	0	1.67	Tnr	AS
ESTEGGPGITR	1	1	1.95E+08	0	-0.447	-0.0995	-0.908	-0.489	-0.339	-0.885	0	-	0	0.333	AA408296	Overlaps intron
ESVLVVPPTPPHPQL	1	5	1.19E+08	1	-0.525	1.14	1.42	0.76	2.06	2.5	0	-	0	NaN	Hrk	Overlaps intron
ETVEECCILAR	1	5	1.49E+08	1	-0.415	0.322	0.531	0.3	-0.0249	0.781	0	-	0	NaN	C130038G02Rik	Overlaps intron
EVAGRSGGR	1	X	1.32E+08	1	-0.316	-0.521	0.293	0.161	0.285	-0.035	0	-	0	NaN	-	Alternative 3' end
EYEEDGSR	1	1	36756941	0	-0.376	0.524	-0.234	0.469	-0.156	0.265	0	-	0	0.474	Actr1b	UCSC
FEDEDFILK	3	5	92235820	0	0	0	0.242	0.195	0.6	0.686	0	-	1	1.67	-	Pseudogene
FLVIMALGMSRAR	4	8	1.09E+08	1	0	0.83	0.376	-0.88	-0.701	-0.137	0	-	0	NaN	Tmco7	AS
FQGPLDWLR	3	18	77462336	1	-0.538	0.756	-0.427	0.339	-0.295	-0.0871	0	-	0	3.12	St8sia5	Overlaps intron
FSDEDATR	1	3	55337524	1	-0.1	1.29	-0.64	-0.386	-0.384	-0.0634	0	-	0	2	Dclk1	UCSC
FSSHNSLLLSPR	1	X	70764755	1	-0.823	-0.796	0.391	0.99	0.353	1.47	0	-	0	2	Atp2b3	AS
FTQAQLDSGLVLFSHR	3	9	56740276	1	-0.807	-0.989	-0.724	0.337	-0.0432	0.547	1	-	0	0.651	Cspg4	UCSC (BLAST)
FWEVISDEHGIDPTGSYHGDSDLQLER	1	12	11889329	0	-0.971	0	1.65	1.65	2.16	1.6	0	-	0	NaN	-	Pseudogene (BLAST)
GAELVDSVLDVVR	5	13	63069659	1	-0.531	0.547	-0.202	-0.123	-0.439	-0.404	1	-	1	0.2	-	Pseudogene (BLAST)
GAHLVSSPAR	1	13	23875947	0	-0.585	-0.3	1.58	2.44	1.9	2	0	-	0	NaN	Trim38	Putative ncRNA
GASQQAVPLR	1	4	1.25E+08	1	-0.844	1.48	-0.872	0.46	1.09	1.45	0	-	0	NaN	Grik3	AS
GDASPAVLR	4	8	96458995	1	-0.31	0.662	-0.0327	-0.304	-0.17	-0.105	0	-	0	0.7	Gnao1	eRNA
GDSVVNLR	3	17	79010529	1	-0.401	-0.521	-0.129	-0.0753	-0.0388	0.491	0	-	0	NaN	Vit	AS
GERGRAGGGR	5	5	1.12E+08	0	-0.585	-0.322	1.14	0.303	0.211	0.35	0	-	0	NaN	-	Putative ncRNA
GFILLRWGWGGGGVGLISR	1	4	1.5E+08	1	-0.556	0.851	0.268	-0.373	-1.17	-0.35	0	-	0	1.33	Rere	Overlaps intron
GGAMQGGLR	2	19	61104526	1	0	1.11	-0.0461	0.0272	0.131	-0.177	0	-	0	1.33	Gprk5	AS

GGDGLGSLTVGLFK	2		7	53669782	1	-0.936	1.5	0.684	0.596	0.563	0.9	0	-	0	NaN	Kcnc1	AS
GGGCVSSALSILSK	1		5	99285415	1	0	0	-0.313	-0.064	-0.181	-0.406	0	-	0	1.93	Bmp3	Overlaps intron
GGGGGGGGGGGGGGGGGGGGGRER	1		9	28395874	1	-0.342	0.12	1.13	0.236	1.35	0.155	0	GGGGGGGGGGGGGGGGGGGGR	0	NaN	Opcml	AS
GGGGGGGGGGRGRGGSR	1		18	12042894	0	-0.485	0.441	0.915	0.983	0.658	0.824	0	-	0	NaN	Cables1	AS
GGHGGIR	4		11	43365085	1	-0.515	1	0.12	0.174	0.292	-0.156	0	-	0	1	Ccnjl	Overlaps intron
GIAILRR	2		2	1.7E+08	0	0	1.22	0.85	0.685	0.762	0.662	0	-	0	NaN	-	Putative ncRNA
GILTGSRR	1		4	1.49E+08	0	-1.46	0.0641	0.446	-0.297	0.453	0.649	0	-	0	NaN	Pik3cd	Overlaps intron
GISYVRR	1		3	1.04E+08	0	-1	1	0.244	0.0279	0.14	0.313	0	-	0	NaN	-	Putative ncRNA
GLAIIRR	5		19	50306195	0	0	2.49	0.85	0.685	0.762	0.662	0	-	0	0.842	Sorcs1	Overlaps intron
GLSYVRR	1		14	21587505	0	-0.279	-1.01	0.244	0.0279	0.14	0.313	0	-	1	NaN	Camk2g	Overlaps intron
GLTLILRR	1		7	20428525	0	-0.522	-1.28	0.137	0.623	0.269	1.69	0	-	0	1.67	-	Putative ncRNA
GLTLLLRR	1		15	23362683	1	0.263	1.49	0.137	0.623	0.269	1.69	0	-	0	NaN	-	Overlaps intron
GMIEALLVR	1		2	22195185	1	0	1.36	0.321	-0.171	0.00606	-0.446	0	-	0	NaN	-	Overlaps intron
GPVTCLPR	1		14	78011663	1	-0.527	1.09	0.623	0.586	0.71	0.126	0	-	1	1.5	D230005D02Rik	Overlaps intron
GSGQVVAQQR	6		14	67529410	0	-0.249	1.04	0.134	0.104	0.458	0.243	1	-	0	NaN	-	Alternative 5' start
GSILASLSTFQQMWISK	1		8	47315377	0	-0.365	-0.975	1.58	0	1.97	1.97	1	-	0	0.647	-	Pseudogene (BLAST)
GSLLSNWACVQLSPGR	1		3	1.33E+08	0	-0.485	0	0.58	0.902	0.642	1.5	0	-	0	NaN	Npnt	Overlaps intron
GSSDEEMPL	2		8	1.22E+08	1	-0.481	-0.667	-0.256	-0.221	-0.279	-0.439	0	-	0	NaN	Cdh13	AS
GTLTDGDSNNQRR	2		9	14412177	0	-0.737	1.35	0.045	0.0787	-0.05	0.242	0	-	0	0.889	Amotl1	Overlaps intron
GVIVRCR	1		3	1.53E+08	0	-0.585	0.29	0.735	0.488	1.11	1.26	0	-	0	NaN	St6galnac3	AS
GVLVRCR	1		17	51925415	0	-0.48	-0.622	0.735	0.488	1.11	1.26	0	-	0	NaN	Satb1	Overlaps intron
GVMVGMGQK	1		19	34326318	0	-0.379	0.692	0.148	0.293	0.61	1.26	0	-	0	NaN	Acta2	UCSC
HELQANCYEEAVKDR	1		10	12566236	0	-0.585	1.49	-0.848	0.988	-0.074	-1.94	0	HELQANCYEE-VKDR	1	NaN	Utrn	Pseudogene
HFECLLSSSPICK	1		9	50798314	0	0.675	0.226	-1.64	-0.0381	0.467	-0.769	0	-	0	NaN	Snf1lk2	Overlaps intron
HGDPGDAAQQEAK	1		1	1.91E+08	0	-0.485	0.515	0.264	-0.0576	-0.0533	-0.09	0	-	0	NaN	LOC100042424	Pseudogene (BLAST)
HPENYQWENWSLENIATILAR	3		1	57439615	1	0.126	-1.12	-0.307	-1.06	1.52	0.785	0	-	0	NaN	1700066M21Rik	UCSC (BLAST)
HSLEGKGCRLLEQNFK	1		15	47903515	0	-0.219	0.34	-1.04	0.472	-0.63	-1	0	-	0	1.8	Csmd3	AS
HSSLIDDMFR	1		14	1.22E+08	1	-0.466	0.93	1.58	0.661	0.152	1.13	1	-	1	0.75	Farp1	Overlaps intron
HTGPEILSMANAGPNTNGSQFFICTSK	2	X		21883037	0	0	0	-0.626	-0.599	0.968	0.299	0	HTGPGILSMANAGPNTNGSQFFICTAK	0	NaN	-	Pseudogene
HTGPGILSMANAGLNTNGSQFFICTAK	1		2	83230557	1	0	0	-0.51	0.693	1.35	1.75	0	HTGPGILSMANAGPNTNGSQFFICTAK	0	NaN	-	Pseudogene
IAKPLSSLTPLIAAAK	5		7	1.05E+08	1	-0.461	-0.69	-0.456	-0.142	0.304	0.299	1	LAKPLSSLTPLILAAK	0	0.317	Pak1	UCSC (BLAST)
IEGDMIICAAYAHELPK	8		6	83551442	0	-0.415	-0.415	-0.0191	-0.227	0.16	-0.118	0	IEGDMIVCAAYAHELPK	0	0.163	-	Pseudogene
IGALSCPRRR	1		12	87860099	1	0	0	0.174	0.226	0.0215	-0.0665	0	-	1	NaN	Esrrb	Overlaps intron
IHFPIAT	3		7	1.07E+08	0	-0.366	1.21	0.412	0.646	0.853	0.877	0	-	0	NaN	-	AS
IIISLAPR	2		6	37869262	1	-0.444	-0.613	0.011	-0.438	-0.0165	-0.102	0	-	0	NaN	Trim24	Overlaps intron
IILMPSLPAR	18		16	38351276	1	0	0	-0.126	0.0985	0.43	0.354	1	-	0	NaN	Cox17	AS
ILAILDAV	1		1	1.54E+08	0	-0.344	-0.328	0	0.834	1.26	1.95	0	-	0	NaN	Rgl1	Overlaps intron
ILDAGNGTIR	1		1	1.73E+08	1	0	0	-0.556	-0.207	0.147	-0.558	0	-	0	NaN	Pvrl4	Overlaps intron
ILDDDTIITTLENLK	13		12	1.12E+08	1	-0.313	3.27	0.478	0.184	0.737	0.352	1	-	0	NaN	Dync1h1	UCSC (BLAST)
ILDDDTIITTLENLKR	7		12	1.12E+08	1	-0.313	3.27	0.478	0.184	0.737	0.352	1	-	0	NaN	Dync1h1	UCSC (BLAST)
ILELDIEDLLLR	3		3	96586664	1	-0.167	-0.752	1.01	0.622	0.912	0.0753	1	-	0	1	Zfp364	Overlaps intron
ILISPLAR	1		1	1.65E+08	0	0.597	0.724	-0.0933	-0.379	-0.206	-0.0539	0	-	0	NaN	Bat2d	AS
ILLLSPAR	1	X		1.09E+08	0	0.447	1.54	-0.0933	-0.379	-0.206	-0.0539	0	-	0	NaN	-	Pseudogene
ILNNLNNILR	1		3	1.07E+08	0	-0.276	0.383	1.13	0.713	0.72	1.22	0	-	0	NaN	-	Putative ncRNA
ILSLLPAR	2		10	79093067	0	-0.485	-0.57	0.011	-0.438	-0.0165	-0.102	0	-	0	NaN	Shc2	Overlaps intron
ILSSPLTFQLLASLAPR	2		1	88138943	1	-0.4	0.505	0.63	-0.462	-1.25	-0.868	1	-	0	NaN	Armc9	Overlaps intron
ILVTLIH	4		13	49058457	0	-0.269	-0.788	0.708	0.837	1.11	-0.578	0	-	0	1.33	BC010304	Overlaps intron
IPGLLGEDLLCGSR	1		16	37956669	1	-0.138	0.541	-0.491	-0.183	-0.705	-0.779	0	-	0	NaN	Gpr156	Overlaps intron
IQSLAEER	1		18	76314644	1	0	1	0.463	0.971	1.16	0.312	0	-	0	NaN	-	Alternative 3' end
IQTMFEQLALVDHPNIVK	1		15	75921106	0	-0.915	-1.36	-0.41	-0.768	0.396	1.55	0	-	1	NaN	-	Alternative 5' start
IRQGMPLILR	1		3	1.47E+08	1	-0.415	0.737	1.13	0.713	0.72	1.22	0	-	0	1.33	Ttll7	Putative ncRNA
IVLLPQDFVIPN	6		1	1.49E+08	1	-0.255	0.376	0.102	-0.104	0.102	-0.0412	0	-	0	NaN	B830045N13Rik	AS
IVVLGIR	2		17	73210269	1	-0.265	-1.27	0.318	0.238	-0.0108	0.134	0	-	0	NaN	-	Alternative 3' end
KLLMMAGIEDCYTSAR	1		2	1.71E+08	0	0	0	0.582	-0.191	0.912	0.249	0	KLLMMAGIDDCYTSAR	0	0.528	-	Pseudogene
KPPPPASPGSSDSSAR	2		8	73438387	1	-0.56	-0.517	1.17	1.03	1.53	1.7	1	-	0	NaN	Mtap1s	UCSC (BLAST)
KQEEQMETEQ	2		4	83109494	0	-0.617	1.04	0.701	0.251	1.31	-0.0514	0	-	0	NaN	Snapc3	UCSC
KTLQLYIQAIDSLA	1		18	69838152	1	-0.11	0.777	1.5	0.971	1.04	1.53	0	-	0	NaN	Tcf4	AS
LAPLMLLPAR	5		13	36301302	1	-0.521	0.278	0.202	0.16	0.684	0.284	0	-	0	2.5	Fars2	AS
LAQVALELK	2		9	1.07E+08	1	-0.186	0.647	0.419	0.0925	0.102	-0.139	0	-	0	3	Vprbp	Overlaps intron
LAVDTEGQRR	1		5	74029635	0	-0.162	-0.467	0.508	-0.946	-0.673	-0.41	0	-	0	1	Sgcb	Overlaps intron
LEDALMENR	2		17	25321158	0	0	0	-0.125	-0.497	-0.215	-0.747	0	-	1	2	-	Novel internal exon
LELMVILLPQTLK	1		2	12896039	1	0	0	1.51	-0.64	1.89	0.634	0	-	1	1	Pter	Putative ncRNA
LFLSPAIQGLLLPAR	2		17	8994702	1	-0.136	1.57	0.259	1.08	0.279	0.217	1	-	1	NaN	Pde10a	Novel internal exon
LGIALNF	15	X		98344394	0	-0.281	-2.02	0.0673	0.027	0.227	-0.0263	0	-	0	3	-	Overlaps intron
LGTESRDTVTENER	1		7	1.41E+08	0	-0.334	-0.103	0.508	0.632	0.369	0.656	0	-	0	1.6	Adam12	Overlaps intron
LIEPVLIQK	15		14	1.23E+08	1	-0.327	-1.57	0.0998	0.146	0.455	0.261	0	-	0	NaN	Zic2	Putative ncRNA
LIGLPLQILM	1		16	76368640	0	-0.681	-0.387	2.28	0	2.58	1.54	0	-	0	2.73	Nrip1	Overlaps intron
LILLGLGDR	1		4	1.01E+08	1	0	0	0.0608	-0.855	1.05	0	0	-	0	NaN	-	Pseudogene
LINDLPAR	1		16	43497573	1	-0.344	0.75	0.613	0.525	0.815	0.501	0	-	0	0.8	-	Overlaps intron

LINISEILK	1		16	40822205	1	0	0	0	0	0	0	0	-	0	NaN		-	Overlaps intron
LIYIEMIIIR	2		2	1.35E+08	1	-0.257	1.34	2.1	0.97	0.785	1.6	0	-	0	NaN		Plcb1	AS
LLAALLHNPQLVER	1		16	31948474	0	-0.427	-1.36	0.204	0.522	0.99	0.902	1	-	1		1.04	0610012G03Rik	UCSC
LLETDLILRN	2		8	84434162	1	-0.485	1.1	0.895	-0.159	0.353	0.798	0	-	0	NaN		Inpp4b	AS
LLLSPLAR	1		3	51960827	0	1	2	-0.0933	-0.379	-0.206	-0.0539	0	-	0		1.2	-	Putative ncRNA
LLLVSSLAPR	1		14	18167137	0	-0.515	0.138	0.429	-0.152	0.207	0.417	0	-	0		1.5	-	Putative ncRNA
LLSIPLAR	1		10	8083470	0	-0.469	0.637	-0.0933	-0.379	-0.206	-0.0539	0	-	0		2	Ust	AS
LLSLIPAR	2		9	74888348	1	-0.163	-0.0675	0.011	-0.438	-0.0165	-0.102	1	-	0		0.75	Arpp19	Overlaps intron
LLSNLSAPR	1		1	68680567	0	-0.302	0.569	0.353	0.35	0.578	0.309	1	-	0	NaN		Erbb4	AS
LLVFLPFILGGP	1		6	50122947	1	-0.5	0.469	0.187	-0.766	-0.599	-0.291	0	-	0		2	Mpp6	Overlaps intron
LLVMVLINR	1		10	69298622	1	-0.516	0.473	1.94	1.11	0.92	0.63	0	-	0	NaN		Ank3	AS
LLWPGGLLLLP	1		4	82096819	0	-0.335	0.8	0.0013	0.16	0.21	0.0826	0	-	0	NaN		Nfib	AS
LNKFYLYICVFTR	1		19	16784133	0	-0.406	0.105	0	3.09	0.895	2.5	0	-	1	NaN		Vps13a	AS
LPPSFLLPAR	5		14	8673935	1	-0.358	1.42	0.202	0.16	0.684	0.284	0	-	0		0.5	Flnb	AS
LTTPTYGDLNHLVSATMSEVTTCLR	127		13	63069299	1	-0.531	0.547	0.292	NaN	0.465	0.39	0	LTTPTYGDLNHLVSATMSGVTTCLR	1	NaN		-	Pseudogene
LVELLLRN	1		13	21289375	1	-0.57	-1.72	1.88	0.734	1.17	1.38	0	-	1	NaN		-	Alternative 3' end
LVIDGKPITIFQER	8		11	3851927	1	0	0	0.506	0.0888	0.611	0.77	1	LVINGKPITIFQER	1	NaN		-	Pseudogene
LVITDVVLNR	1		2	1.58E+08	0	-1.29	-0.316	0.908	-0.17	0.659	0.571	1	-	0	NaN		-	Overlaps intron
LYIVFSLLILCR	2		3	97557685	0	-0.0849	0.976	-0.469	0.132	0.659	-0.588	0	-	0	NaN		Pde4dip	Overlaps intron
MDSFDEDLAR	2		4	1.26E+08	0	-0.204	0.824	0.662	-0.237	0.571	0.756	1	-	0		0.667	Thrap3	UCSC
MFQYDSTHGK	4		11	99539579	1	0.517	0	0.382	0.127	0.927	0.9	1	-	0		0.6	-	UCSC (BLAST)
MSIFGH	4		1	1.79E+08	0	-0.384	0.425	-0.231	0.353	0.227	0.408	0	-	0		2	-	Overlaps intron
MVILELRR	1		15	76514928	1	-0.49	-1.19	-1.03	0.0759	-0.0338	-1.56	0	-	0	NaN		Ppp1r16a	AS
MVVSEEYHLSSISK	1		5	1.06E+08	1	-0.516	0.765	0.404	-0.64	-0.716	-0.515	0	-	0	NaN		Zfp326	AS
NAFLSSSALDK	3		19	12534993	0	1.58	0	0.159	0.595	0.81	0.457	0	-	0		4	-	Alternative 3' end
NALQELQQIIITPIK	6		7	29191631	0	-0.259	0.147	0.656	-0.18	0.617	0.429	1	-	0	NaN		Samd4b	UCSC (BLAST)
NCLPGLQLQEESTGLER	3		19	3819420	0	0	0	-1.18	0.569	0.919	2.49	1	-	0		1	-	Alternative 3' end
NDSDSVLISILEK	1		3	35805209	0	-0.617	-0.226	-0.984	0.0322	-0.412	0.346	0	-	0	NaN		Dcun1d1	Overlaps intron
NLISAGGQGPR	1		8	1.25E+08	1	-1.22	0.193	0.731	0.27	0.402	1.34	1	-	0	NaN		Zfpm1	Overlaps intron
NMETPLSVHHCFVK	1		3	37122645	0	-1.32	0	-0.35	0.737	-2.67	-1.77	0	-	0	NaN		Il21	Putative ncRNA
NSNILMENR	2		4	49601752	0	-0.48	-1.18	-0.131	-0.514	-0.184	-0.763	0	-	0		1.29	2810432L12Rik	AS
NSSYFVEWIPNDVK	17		4	24166130	1	0.649	-1.64	0.562	0.507	0.24	0.547	1	NSSYFVEWIPNNVK	0		0.714	-	Pseudogene
NVELTYYFLFHLVILAR	1		14	1.18E+08	1	-0.33	0.916	-0.0119	0.0148	-0.157	0.675	0	-	0	NaN		Gpc6	Overlaps intron
NVVHQLSVTLEDLYDGATR	12		5	21458463	0	-0.469	0.222	0.836	1.72	0.987	0.721	1	NVVHQLSVTLEDLYNGATR	0	NaN		Reln	Pseudogene
PFSPLMENR	1		9	1.17E+08	0	-0.441	0.559	0	-0.21	-0.742	-0.966	0	-	0	NaN		Rbms3	AS
PLCILTGCQPLR	1		14	29813217	0	-0.497	0.503	0.105	0.466	0.527	1.12	0	-	0		2.18	Cacna2d3	Overlaps intron
QARSLDPLALIR	1		4	1.4E+08	0	-0.238	0.258	-1.58	1.02	0.36	2.73	0	-	0		2.71	Igsf21	Divergent
QCWKMLQMASGYGTTMR	1		1	68551590	0	-0.302	0.569	-0.269	-0.684	0	0.731	0	-	0		4.73	Erbb4	Overlaps intron
QDLDVAR	1	X		35701835	0	0	1	0.851	0.881	0.462	0.389	0	-	0	NaN		-	Putative ncRNA
QEAVAGSLSK	4		12	59839129	0	-0.367	0.268	0.401	0.272	0.239	-0.0952	0	-	0	NaN		-	Putative ncRNA
QEFDTMEDHAGDYTLLQDQEGDMDHGLK	1		11	1.04E+08	1	-0.648	0.159	-0.717	0	1.72	0.862	0	-	0	NaN		Mapt	UCSC (BLAST)
QGAEELAR	1		15	59195487	0	-0.295	1.35	1.74	1.58	2.85	0	0	-	0	NaN		E430025E21Rik	Overlaps intron
QGLILYLR	1		9	56157990	0	-0.57	0.595	0	0	0	0	0	-	0	NaN		C230081A13Rik	AS
QIIEINPR	1		11	47353320	0	-0.459	-0.25	1.19	0.404	1.15	0.831	0	-	0	NaN		-	Pseudogene
QLALEEQHER	2		5	1.22E+08	1	-0.533	-0.115	0.311	1.01	0.709	-0.0069	1	-	0		0.5	EG545802	UCSC
QNNILIVANNSCVLK	1		1	74490131	0	1.08	0.113	0.889	-0.0544	2.04	0.48	0	-	0		4	Usp37	AS
QPALGTALK	5		17	27624222	0	-0.628	1.2	0.193	0.0447	0.425	-0.0162	0	-	0	NaN		Grm4	AS
QPTHLPR	1		8	1.22E+08	1	-0.531	-0.305	-0.861	0.357	-2.23	0.357	0	-	0	NaN		Usp10	AS
QQVLLTMSEAPACK	2		9	67118687	0	-0.55	0.0687	0.215	0.0109	0.351	0.973	0	-	0	NaN		Tln2	AS
QTERGGGGGGGGGGGGGGGR	1		14	30226844	0	-0.497	0.503	-0.365	-0.0292	-0.376	-0.265	0	-	0	NaN		Cacna2d3	AS
RAPADTHSSSAESIEGSPR	1		1	91478172	1	-0.613	0.648	0.482	0.256	-0.243	-1.09	0	-	1	NaN		Centg2	Novel internal exon
RASGEPSVESSR	19		14	67529332	0	-0.249	1.04	-0.186	0.187	0.739	-0.126	1	-	0		0.909	-	Alternative 5' start
RIEAGSCPR	1		5	1.22E+08	0	-0.519	1.33	0.991	1.27	0.747	0.308	0	-	0	NaN		Ptpn11	Overlaps intron
RLCQGSIVEIIK	2		16	40798627	1	0	0	0.544	-0.624	0.286	0.319	0	-	0	NaN		-	AS
RLESCAPR	2		1	1.9E+08	1	-0.485	0.893	0.496	0.633	0.374	0.154	0	-	0		0.5	-	Putative ncRNA
RPETVIGVDINPYLHMR	1		9	1.22E+08	0	-0.652	-0.0265	0.159	-0.951	-1.22	0.954	0	-	0	NaN		Tmem16k	Alternative 3' end
RQLGNNLLLR	1	X		74870093	1	-0.0498	-0.22	1.13	0.713	0.72	1.22	0	-	0		2	Tbl1x	Overlaps intron
RQQLQELR	1		5	1.44E+08	0	-0.697	-1.05	0.729	1.05	0.547	0.614	0	-	0		1.5	Fbxl18	AS
RRVLELGDLER	1		3	1.23E+08	0	0	0	0	0	0	0	0	-	0	NaN		Synpo2	Overlaps intron
SAPADGADLSAHLWAR	1		14	31944491	0	0	0	0.000787	-0.117	-0.18	0.722	1	-	1	NaN		-	Alternative 5' start
SCSLLVLNLK	1		14	12560810	1	-0.48	1.42	1.82	0.347	0.748	0.0342	0	-	0		1.67	Ptprg	AS
SDLHALVVASSVPLLFR	1		8	1.27E+08	1	-0.39	-0.788	0.17	0.0297	1.14	-0.585	1	-	0		1.21	AK122209	UCSC (BLAST)
SHFEQWGTLTNCVVMR	5	X		1.39E+08	1	0	0	0.282	0.435	1.37	0.426	0	-	0	NaN		-	UCSC (BLAST)
SIVETLVLSPSTVGSGR	1		19	45796161	0	0	0	3.89	3.85	0	1.58	0	-	0	NaN		-	Putative ncRNA
SLFDFLLSRN	5		1	32403440	1	-0.302	0.474	0.988	0.0747	-0.467	0.0576	0	-	0	NaN		Khdrbs2	AS
SLFSSPASLAFPYSPVAR	12		14	1.04E+08	1	-0.364	1.18	0.0889	0.661	-0.00528	0.00626	1	-	1	NaN		Slain1	UCSC
SMTEAEQQQLIDDHFLFDKPVSPLLASSMAR	2		16	38483886	1	0.29	0	-0.346	-0.502	-0.305	-1.18	0	SMTEAEQQQLIDDHFLFDKPVSPLLLASGMAR	1	NaN		Cd80	Pseudogene
SRVGLAEAER	1		8	75251940	1	-0.167	-1.06	0.0241	0.652	0.994	0.554	0	-	0	NaN		Sin3b	Overlaps intron
SSSWLVVQSLEAR	9		11	81715748	0	-0.507	-0.111	-0.155	-0.188	0.243	0.0834	0	-	0	NaN		Accn1	Overlaps intron

STYEDQSAR	1	6	71833517	0	-0.472	-0.253	0.0724	-0.454	-0.231	-0.753	0	-	0	0.526	Ptcd3	UCSC
TEGRETGGRER	3	16	63563279	0	0.142	0.624	0.0783	0.402	0.0597	-0.26	0	-	0	1.62	Epha3	AS
TFCVFILTLR	5	X	72401812	0	-0.415	-1	1.1	-0.322	0.494	-0.145	0	-	0	NaN	4930428E23Rik	Pseudogene
TFSVMPSPK	3	13	63069500	1	-0.531	0.547	-0.0663	-0.0996	0.253	0.285	0	-	1	0.312	-	Pseudogene
TGSGFTSLLMER	3	2	1.51E+08	1	-1.54	-3.41	-0.0586	-0.0585	0.0611	-0.558	1	-	0	0.25	-	Pseudogene (BLAST)
TIDFDSLSVGR	8	14	67529440	0	-0.249	1.04	0.101	0.169	0.273	0.282	1	-	0	0.719	-	Alternative 5' start
TLILGH	1	1	95590235	0	-0.688	-1.53	0.392	-0.213	0.175	-0.575	0	-	0	NaN	Bok	Overlaps intron
TLLIGH	1	6	1.11E+08	1	-0.439	0.561	0.392	-0.213	0.175	-0.575	0	-	0	NaN	Grm7	Overlaps intron
TLQAEQFIVYRLDQKAK	2	12	76925629	1	-0.444	1.45	0.181	0.806	1.1	1.58	0	-	0	3.5	Syne2	Overlaps intron
TLSQITITNR	1	13	18082330	0	-0.737	-0.152	0.725	-0.589	-0.585	-0.567	0	-	0	NaN	1600012F09Rik	Putative ncRNA
TLWASVQLLLTLISK	1	11	69727257	1	-0.467	0.0332	0.713	0.454	0.0863	0.179	0	-	1	2	0610025P10Rik	Alternative 3' end
TRLSSDSQSSACFCLLR	1	12	33692187	0	0	0	1.25	0	2.16	1.66	0	-	0	NaN	-	Putative ncRNA
TSFLEMLMGALLLVISDCCLLVCSFLPPHSGAGEFQL	1	2	74632604	0	-1.58	0	-0.737	0	0.642	1.46	0	LLHLKDRCLISCSVLSPRAGARELGEFH	0	2.91	-	Putative ncRNA
TSTVDLPIESQLLWQLDR	14	11	53080494	0	1.11	2.23	0.455	0.68	0.612	0.526	1	-	0	0.525	Hspa4	UCSC (BLAST)
TTSMNLARNVHIIMPISK	1	4	19987497	1	0.298	-0.361	-0.717	-0.649	-0.668	0.147	0	-	0	1	LOC667301	Overlaps intron
VAEVLFDAADANAIEEVNLAYENVK	4	12	1.12E+08	1	-0.313	3.27	1.72	1.84	1.03	2.29	0	-	0	NaN	Dync1h1	UCSC (BLAST)
VAILFLALVSVLGAQS	1	11	56929950	1	-0.641	0.342	0.933	1.64	2.78	1.38	0	-	0	1.52	Gria1	AS
VAVLQALASTVNR	7	6	71855088	0	-0.328	0.142	0.267	0.636	0.425	0.284	1	-	0	NaN	Ptcd3	UCSC (BLAST)
VDNDEDEHQLSLR	1	10	27000624	0	0	0	1.39	-0.3	0.732	0.0626	0	-	0	NaN	Lama2	AS
VEEQVFPLLDLR	1	13	21360267	0	0	0	2.12	0.785	1.48	2.37	0	-	1	NaN	-	Putative ncRNA
VGLLLVFPLIQSQSR	3	5	1.22E+08	1	-0.533	-0.115	0.885	1.08	1.52	0.613	0	-	0	NaN	EG545802	UCSC (BLAST)
VIHDNFGIAEGLMTMVHAITATQK	1	8	89183665	1	-0.607	0.693	2.83	3.93	2.07	3.02	0	IIHDNFGIMEGLMTMVHAITATQK	1	NaN	Lonp2	Putative ncRNA
VIHDNFGIVEGLMTTVCAITATQK	6	9	1.1E+08	0	-0.472	-1.18	0.346	0.33	0.168	-0.0471	0	VIHDNFGIVEGLMTTVHAITATQK	1	NaN	-	Pseudogene
VIHDNFGIVEGLMTTVHGITATQK	12	14	1.04E+08	1	0	0	0.857	0.882	1.17	0.829	0	VIHDNFGIVEGLMTTVHAITATQK	1	NaN	-	Pseudogene
VIIILWLK	1	14	62005615	0	-0.0589	-0.447	0.584	0.53	-0.208	0.256	0	-	0	NaN	Kpna3	Overlaps intron
VIISTPSANAPMFVMGVNHEK	3	11	1.09E+08	0	0	0	1.09	0.97	0.721	1.31	0	-	0	NaN	-	Pseudogene (BLAST)
VILLVV	1	1	1.33E+08	0	-0.778	-1	0	0	0	0	0	-	0	NaN	Srgap2	Overlaps intron
VILLVVVMGMGNLR	1	9	47671285	1	-0.429	0.555	-2.75	-3.08	-0.142	-2.24	0	-	0	NaN	-	AS
VIPELDGK	2	11	3852386	1	0	0	0	0	0	0	0	-	1	NaN	-	Pseudogene
VLIHLAK	2	5	40139120	0	-0.459	1.52	0.127	0.0743	0.204	-0.283	0	-	0	NaN	Hs3st1	Overlaps intron
VLIIWILK	5	3	1.14E+08	1	-0.263	1.42	0.416	0.354	0.467	0.585	0	-	0	NaN	Col11a1	AS
VLLHLAK	2	5	1.02E+08	0	-0.354	1.44	0.127	0.0743	0.204	-0.283	0	-	0	1.14	Wdfy3	Overlaps intron
VLLIWIK	1	19	58945723	0	-0.566	-1.69	0.584	0.53	-0.208	0.256	0	-	1	NaN	-	Alternative 5' start
VLLLWLLK	2	18	46761781	1	-0.276	-0.769	0.416	0.354	0.467	0.585	0	-	0	NaN	Eif1a	Overlaps intron
VLTISLLGH	1	6	98988990	0	-0.459	-0.372	0	0	0	1.79	0	-	0	NaN	Foxp1	Overlaps intron
VSQHFPGEDVLQRTR	1	5	1.13E+08	0	-0.556	-0.286	-0.408	0.241	0.24	0.579	0	-	0	NaN	Myo18b	AS
VTHTVPIYEGYALPHAILR	8	13	81204153	0	-0.263	1.12	1.04	0.865	0.732	0.727	1	-	0	0.188	-	Pseudogene (BLAST)
VTSIILLMFS	1	5	5563174	0	-1	1.58	0	0	0	-2.65	0	-	0	NaN	-	Divergent
VVDLLACR	2	X	1.31E+08	0	0.286	-0.965	0.975	1.05	0.399	-0.621	0	-	0	NaN	Btk	AS
VWVSQGSDAPR	1	15	80226262	1	-0.62	-1.45	-1.32	-1.34	-0.531	-1.6	0	-	0	NaN	Cacna1i	Alternative 3' end
WEGGMQRGGGGMGGGSER	1	16	81459937	1	-0.349	0.836	0.973	0.76	0.314	0.681	0	-	0	NaN	Ncam2	AS
WMADDLR	2	16	59592942	0	0	2	1.22	1.34	1.54	1.2	0	-	0	1	LOC672884	AS
WWGRGGEGVGVGVGVGEGWGRLGEGR	1	5	89346189	1	-0.389	0.134	-0.146	0.0525	1.09	0.678	0	-	0	NaN	Slc4a4	Overlaps intron
YNAAGTGLQVEDCR	1	19	59990938	0	-0.494	-1.93	0.0855	-0.103	-0.00075	0.0826	0	-	0	NaN	Rab11fip2	Overlaps intron

Supplementary Table 1. The table lists all of high-quality novel peptides which were mapped to the RNA-seq database

GIAILRR	GLAIIRR
GISYVRR	GLSYVRR
GLTLILRR	GLTLLLRR
GVIVRCR	GVLVRCR
ILISPLAR	ILLLSPAR
TLILGH	TLLIGH
VLIIWILK	VLLLWLLK

Supplementary Table 2. The table lists the seven pairs of peptides which matched two different non-coding RNAs that differed only by an isobaric I/L amino acid, while the unambiguous identification of the source of these peptides is not possible, it is clear that these peptide sequences are not found in the canonical mouse protein sequences.

Supplementary Table 3

	PCR Region	Forward Primer	Reverse Primer
1	Farp1, novel intron region 1	GCT GGA GGC AGT AGC AAT TC	CGT CTC ATC CTT CCT CTT GC
2	Farp1, novel intron region 2	GGG TTG CCA CAG AGA AGG TC	CAC CAT GGC TGA TGG AGA AA
3	Farp 1, novel intron region 3	TAG GAG CCT TCT GTG GCT GT	GAG GTC TCA GGA AGC CCT CT
4	Suvn, alternative 3' end	GCC AAA CTG TCA CCC AAA CCC	TTC ACA TCT CCC CAA ACC TC
5	Armc9, intron retention	CCC ATG GTT CAT CTG CTC TT	GCT GGT TAC TAG CGG AGA CG
6	Grpbp10, divergent	CAT GCA TGT TAT CCC AGC AC	TAT GGA GCC AGT GGT TGA CA
7	Elmo2, divergent	CCC AGC AAG CTA AGA AGT GC	TCT GGT GTG CCT CAC TCT TG
8	E130006D01 Rik, overlaps intron of annotated ncRNA	GTA AGC TGC AGG CAC ATC AA	CTT CAT GGC AGA ACC TGG AT
9	Cacna2d3, AS	CTG GGT TGG CAA GAA CAA AT	CGG TTC CCA GGT AAT AGC AA
10	Gprk5, AS	GGA AGA ATC ATG GGC ACT GT	TAT CAG CCT GAC CTG GGA AG
11	Nars2, AS	CAT GCA CAC AAT GGA CAC AA	TGG CAG TGG ATG TAG CTC AG
12	Cox17, AS	AGG ACA CAC CAC CCT AGT CG	TCT CCA GAC CAG AGG CAC TT
13	Mlstd2, AS	TAA GCA GCA GCA AAG GGA AT	CTG GGC CCT CTC TCT CTT TT
14	Fars2, AS	ACC CTC ACT GGG ACT CCT CT	TTC AGC AAG GTG TCA GAT GC
15	St6galnac3, AS	TCC AGT GTG CCA ACA TTC AT	CAC CAT CCC TGT CAC TCT CA
16	PGOMOU00000135506, pseudogene	AAT GGT GAA GGT CAG TGT GAAC	ACT CCT TGG AGG CCA TGT AG
17	PGOMOU00000135766, pseudogene	AAT GGT GAA GGT CGG TGT G	TAC TCC TTG GAG GCC ATG TAG

Supplementary Table 3. The table lists the regions of interest and primers sequences that were designed to verify the expression of 14 anti-sense RNAs (Supplementary Figure 6B) along with 3 novel intron regions of FARP1 (Figure 2C) by RT-PCR.